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(54) Title: SPECIFIC MARKERS FOR PANCREATIC CANCER

(57) Abstract: The present invention provides polypeptides which are up- or down-regulated in pancreatic cancer and which can be used as markers for diagnosis of pancreatic cancer. The invention also provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of a) obtaining a biological sample; and b) detecting and/or measuring the increase of one or more polypeptides as disclosed herein. Furthermore, screening methods relating to inhibitors and antagonists of the specific polypeptides disclosed herein are provided.

Specific Markers for Pancreatic Cancer

The present invention relates to markers for diagnosis of pancreatic cancer comprising at least one polypeptide identified by proteomics to be up-regulated in pancreatic cancer, to an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of a) obtaining a biological

5   sample; and b) detecting and/or measuring the increase of specific markers as disclosed herein. Furthermore, screening methods relating to antagonists of the specific markers disclosed herein are provided.

10 Pancreatic cancer is a common cause of death in the Western world. It is one of the most aggressive malignant tumors, with an overall 5-year survival rate of 0.4%. In many patients with pancreatic cancer, accurate preoperative diagnosis is difficult to achieve with conventional imaging analyses. Most patients with pancreatic cancer present late in the course of the disease and have either locally extensive or metastatic disease. Overall,

15 only up to 20% are candidates for resection and have the potential for curative surgery. Among the causes for this late presentation is the lack of diagnostic methods for an earlier detection of the disease. Besides this lack of diagnostic methods, the high mortality of patients with pancreatic cancer is additionally caused by a lack of effective treatments. Therefore, the identification of new targets for early diagnosis of pancreatic tumors, and

20 for the development of agents to treat pancreatic cancer is a challenge of paramount importance.

25 The problem of identifying polypeptides suitable as markers of pancreatic cancer for early diagnosis of the disease, and the long felt need for such markers, was overcome by the present invention by applying the new technology of proteomics. It was surprisingly found by using proteomic technology that a specific set of polypeptides are differentially expressed in pancreatic tissue obtained from individuals suffering from

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pancreatic cancer, as compared to healthy pancreatic tissue. Said differentially expressed polypeptides are listed in appended tables 2 and 3. The polypeptides in table 3 are encoded by genes which were previously identified to be up-regulated in pancreatic cancer on the transcriptional level (Iacobuzio-Donahue et al., (2002). Am. J. Pathol. 160, 1239-1249). However, it is well known that regulation on the transcriptional level is not necessarily indicative of a similar regulation of the expression of the respective gene on the translational level. Thus, only by demonstrating that the polypeptides listed in table 3 are up-regulated in pancreatic cancer is it possible to use them for polypeptide-based diagnostic assays for the detection of pancreatic cancer.

Based on the polypeptides listed in tables 2 and 3, the present invention provides a marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in tables 2 and/or 3 (Seq ID No. 1 to 24 and 26 to 49; and/or Seq ID No. 25 and 50 to 55). Thus, the term "marker" as used herein refers to one or more polypeptides that are regulated in cancer and that can be used to diagnose pancreatic cancer or a susceptibility to pancreatic cancer either alone or as combinations of multiple polypeptides that are known to be regulated in pancreatic cancer. Preferably, said polypeptides are selected from the group consisting of Seq. ID No. 2 to 10, 12 to 15, 17, 19, 20, 23, 24, 27, 28, 31 to 40, 42 to 45, 47 and 48; and/or Seq ID No. 50 to 54. More preferably, said polypeptides are selected from the group consisting of Seq ID No. 3, 4, 6, 9, 14, 15, 27, 31 to 35, 37, 39, 40; and/or Seq ID No. 50 to 52. Even more preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 9, 14, 15, 31, 33 to 35 and/or Seq ID No. 51 and 52. Most preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 14, 15 and 31; and/or Seq ID No. 52.

The term "polypeptide" as used herein, refers to a polymer of amino acids, and not to a specific length. Thus, peptides, oligopeptides and proteins are included within the definition of polypeptide.

Preferably, the marker of this invention is a marker comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 2.

Furthermore, a polypeptide selected from the group consisting of the polypeptides listed in tables 2 and/or 3, is used as a marker or as part of a marker for diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer. Preferably, said polypeptides are selected from the group consisting of Seq. ID No. 2 to 10, 12 to 15, 17, 19, 20, 23, 24, 27, 28, 31 to 40, 42 to 45, 47 and 48 from table 2 and/or Seq ID No. 25 and 50 to 54 from table 3. These polypeptides are induced at least two fold, as can be seen in tables 2 and 3. More preferably, said polypeptides are selected from the group consisting of Seq ID No. 3, 4, 6, 9, 14, 15, 27, 31 to 35, 37, 39, 40 from table 2 and/or Seq ID No. 50 to 52 from table 3. These polypeptides are induced at least three fold, as can be seen in tables 2 and 3. Even more preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 9, 14, 15, 31, 33 to 35 from table 2 and/or Seq ID No. 51 and 52 from table 3. These polypeptides are induced at least 4 fold, as can be seen in tables 2 and 3. Most preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 14, 15 and 31 from table 2 and/or Seq ID No. 52 from table 3, which are the polypeptides that are induced five fold, as shown in tables 2 and 3.

The present invention pertains to a marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 6. Preferably, said at least one polypeptide additionally does not include Seq ID No.s 25 and 50 to 55.

In a preferred embodiment, the marker hereinbefore described additionally comprises at least one of the polypeptides listed in table 5.

Several groups of polypeptides were identified as markers for pancreatic cancers:

Enzymes

One of the enzymes that caught our attention was Glutamine γ-glutamyltransferase/tissue transglutaminase (TGLC, Seq ID No. 54). It is a member of the transglutaminase family that catalyzes Ca2+ dependent reactions resulting in the post translational modification (cross-linking and conjugation with polyamines) of proteins at

the level of glutamine and lysine residues (Greenberg, C. S., Birckbichler, P. J., and Rice, R. H. Transglutaminases: multifunctional cross-linking enzymes that stabilize tissues. FASEB J., 5: 3071-3077, 1991). Many different roles for this protein have been described, among them apoptosis, adhesion, and differentiation (Amendola, A., Fesus, L., Piacentini, M., and Szondy, Z. "Tissue" transglutaminase in AIDS. J.Immunol.Methods, 265: 145-159, 2002). There is some controversy on the role of TGLC in apoptosis. While several pieces of evidence suggest that TGLC is a pro-apoptotic protein (Melino, G., et al., Mol.Cell Biol., 14: 6584-6596, 1994), Jason et al. found that TGLC acts in anti-apoptotic fashion (Boehm, J. E., et al.J.Biol.Chem., 277: 20127-20130, 2002). Many substrates of TGLC are major extra-cellular matrix (ECM) components such as fibronectin, osteonectin, and collagen, which makes TGLC an important enzyme in ECM development (Raghunath, M., et al., J.Clin.Invest, 98: 1174-1184, 1996, Nemes, Z., Jr., et al. J.Biol.Chem., 272: 20577-20583, 1997). Abnormal ECM development is involved in many pathological conditions such as fibrosis and may play a role in the proliferation of fibrous tissue observed in PC. Haroon et al. described that TGLC ECM-promoting abilities are an important part of the host response mechanism against tumor growth (Haroon, Z. A., et al, Lab Invest, 79: 1679-1686, 1999). Interestingly, loss of TGLC can be a biomarker for prostate adenocarcinoma (Birckbichler, P. J., et al., Cancer, 89: 412-423, 2000), which raises the question whether the measured TGLC is produced by neoplastic ductal cells and/or stromal cells. Measurements of mRNA levels in PC, normal tissue and PC cell lines indicate that TGLC is over expressed in both cell types (Iacobuzio-Donahue, C. A., et al., Am.J.Pathol., 160: 1239-1249, 2002), which would distinguish PC from prostate adenocarcinoma. Therefore, one preferred embodiment of the present invention is a marker comprising Seq ID No. 54.

Cytoskeletal proteins

Several cytoskeletal proteins were detected at higher levels in PC than in surrounding tissue. One of these is gelsolin (Seq ID No. 3), a Ca^{2+} and PIP2 (polyphosphoinositide 4,5-bisphosphate) regulated severing and capping protein, which is a multifunctional actin regulatory protein and has roles in actin remodeling, motility, signaling, apoptosis and cancer (Maruta, H. G proteins cytoskeleton and cancer. Austin, Tex.: R.G. Landes, 1998). In several cancer studies, gelsolin expression has been described as down-regulated during carcinogenesis (breast, colon, stomach, bladder, prostate, and lung) (Asch, H. L., et al., Cancer Res, 56: 4841-4845, 1996; Dosaka-Akita, H., et al., Cancer Res, 58: 322-327, 1998, Prasad, S. C., et al. Electrophoresis, 18: 629-637, 1997). Another example for an up-regulated cytoskeletal protein is fascin (Seq ID No. 58), an

actin-bundling protein that has a role in cell matrix adhesion, cell interaction and migration. Fascin over expression has been reported in several cancers, such as breast, colon, and ovarian carcinoma (29). The present invention also features fascin 2 as a polypeptide up-regulated in pancreatic cancer (Seq ID No. 56). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 3. In another preferred embodiment, the marker comprises Seq. ID No. 58. In another preferred embodiment, the marker comprises Seq. ID No. 56.

In our study, cytokeratin 7 (Seq. ID No. 52) and cytokeratin 19 (Seq ID No. 33) showed strong expression in PC. Both have also been described in other cancers and have been linked with metastasis formation (Moll, R., Int.J.Biol.Markers, 9: 63-69, 1994.). High protein levels of actinin-4 (Seq ID No. 5) were detected in PC. This protein was linked by others with cell motility and cancer invasion (Honda, K., Yamada, T., Endo, R., Ino, Y., Gotoh, M., Tsuda, H., Yamada, Y., Chiba, H., and Hirohashi, S. J.Cell Biol., 140: 1383-1393, 1998.). Taken together, the apparent strong expression of cytoskeletal proteins is likely to be an important factor in the strong invasiveness and metastasis-forming potential of PC. Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 52. In another preferred embodiment, the marker comprises Seq. ID No. 33. In another preferred embodiment, the marker comprises Seq. ID No. 5.

Metastasis

Cancer of exocrine pancreas is characterized by extensive local invasion, early lymphatic and hematogenous metastasis. Metastasis in PC has been found in the skeleton, eye, bladder, etc. The extent of angiogenesis depends on the balance between pro-angiogenic or anti-angiogenic factors released from cancer and host cell. Currently, intratumoral microvessel density (IMD) measured by immunocytochemistry appears to be the most reliable parameter for assessing angiogenic activity. Patients with high IMD have decreased survival rates in a variety of cancers (Fujioka, S., et al, Cancer, 92: 1788-1797, 2001). Thymidine phosphorylase (TYPH or TP, Seq ID No. 31) which is identical to platelet-derived endothelial cell growth factor, is strongly expressed in PC and stimulates the chemotaxis of endothelial cells through the 2-deoxy-D-ribose, degradation products of thymidine by TP, thus indirectly inducing angiogenesis (Haraguchi, M., et al. Nature, 368: 198, 1994.). Shuichi Fujioka et al. found that IMD and TP status were independent predictive indicators for overall as well as relapse-free survival in PC (Fujioka, S., et al., Cancer, 92: 1788-1797, 2001). An additional protein detected at higher levels in PC than in surrounding tissue likely involved in metastasis formation is

osteoblast specific factor 2 (Seq ID No.53), a putative bone adhesion protein. Breast carcinoma commonly metastasizes to bone (Guise, T. A. Cancer, 88: 2892-2898, 2000). Although the role of this protein in PC is not clearly established, our findings suggest a similar role for osteoblast specific factor 2 in PC. Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 31. In another preferred embodiment, the marker comprises Seq. ID No. 53.

Small GTP-binding proteins

Four small GTP-binding proteins and interacting proteins were more strongly expressed in PC than in normal pancreas tissue. These include RAN (Seq. ID No. 27), GBLP (guanine nucleotide binding protein β subunit-like protein RACK1, Seq. ID No. 47), GDIR (Rho GDP dissociation inhibitor 1, Seq. ID No. 55), and IQG1 or IQGAP1 (Ras gtpase activating like protein, Seq ID No. 25). Small GTP-binding proteins constitute a superfamily, which is structurally classified into at least five families: the Ras, Rho, Rab, Sar1/Arf, and Ran families and are involved in the regulation of gene expression, cytoskeletal reorganization, and nucleocytoplasmic transport (Takai, Y., et al Physiol Rev., 81: 153-208, 2001). RAN is known to enhance androgen receptor-mediated transactivation and was shown to be overexpressed in prostate cancer (Sampson, E. R., et al., J.Biol.Regul.Homeost.Agents, 15: 123-129, 2001). Increased expression of RAN in 81% of prostate tumor cases, may contribute to over proliferation of prostate tumor cells (Li, P., et al, Am J Pathol, 161: 1467-1474,2002). GBLP is an anchoring protein for activated protein kinase Cβ and a variety of other proteins. Protein kinase C plays an important role in angiogenesis and cancer growth. Berns et al. found GBLP up-regulated in during angiogenesis in vitro and also associated with nonendothelial cells in angiogenically active tissue (Berns, H., et al., FASEB J., 14: 2549-2558, 2000). Further more, mRNA expression of GBLP is detected in epithelial cells of human colon carcinoma and proliferating epithelial cell of normal colon tissue. Therefore, there is a likely link between high GBLP expression and tumor growth. GDIR (Rho GDP dissociation inhibitor) had been found up-regulated in a chemoresistant fibrosarcoma cell line by 2D-PAGE (Sinha, P., et al., Electrophoresis, 20: 2961-2969, 1999) and may block apoptotic signal pathway mediated by Ras and c-jun kinase, resulting in the increase resistance against environmental stress. IQG1 (Ras GTPase-activating-like protein) is a widely expressed 190-kDa Cdc42-, Rac1-, and calmodulin-binding protein that interacts with F-actin in vivo and that can cross-link F-actin microfilaments in vitro. IQG1 negatively regulates the Ecc-based (E-cadherin/catenin complex) cell-cell adhesion by dissociating alpha-catenin. Up-regulation of IQGAP1 is correlated with the malignant

phenotype in gastric cancer (Sugimoto, N., et al., J. Hum. Genet, 46: 21-25, 2001). By immunohistochemical analysis, IQGAP1 was found overexpressed in colorectal carcinoma and associated with carcinoma invasion (Nabeshima, K., et al, Cancer Lett, 176: 101-109, 2002). Since cancer invasiveness is associated with the localized disruption of cell-cell adhesion, both our results and Iacobuzio-Donahue et al.'s data suggest that IQGAP1 may be involved in the disruption of local adhesion and in PC invasion to surrounding tissue. Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 27. In another preferred embodiment, the marker comprises Seq. ID No. 47. In another preferred embodiment, the marker comprises Seq. ID No. 55. In another preferred embodiment, the marker comprises Seq. ID No. 25.

S100 protein family

Another protein with high-level expression in PC is S109 (S100A9, MRP-14, calgranulin B, Seq ID No. 49), a member of the S100 protein family of highly homologous low molecular weight calcium binding proteins. Calgranulins are characterized by cell type-specific expression in cells of epithelial, myeloid and endothelial origin and accumulation at sites of acute and chronic inflammation (e.g. rheumatoid arthritis, cystic fibrosis, psoriasis, allergic dermatitis, inflammatory bowel diseases) (Donato, R. Int.J.Biochem.Cell Biol., 33: 637-668, 2001). S100A8 and S100A9 can form a noncovalent heterodimer protein complex called calprotectin. Current reports support that both of S100A9 and S100 A8 have wide range of possible intracellular as well as extracellular functions (Schafer, B. W. and Heizmann, C. W. Trends Biochem.Sci., 21: 134-140, 1996). S100A8 and S100A9 are negatively regulated by glucocorticoids in a c-Fos-dependent manner and over expressed throughout skin carcinogenesis (Gebhardt, C., et al., Oncogene, 21: 4266-4276, 2002). These proteins are also more strongly expressed in colorectal carcinoma than in matched normal colon mucosa, as shown by proteomics analysis (Stulik, J., et al., Electrophoresis, 20: 1047-1054, 1999). S100A9 has been detected in cultured human adenocarcinoma (AC) cells derived from various organs, and is associated with tumor differentiation in pulmonary adenocarcinoma (Arai, K., et al., Oncol.Rep, 8: 591-596, 2001). Iacobuzio-Donahue et al's work indicates that over expression of S100A4 in PC is associated with poor differentiation and DNA hypomethylation (Rosty, C., et al., Am.J.Pathol., 160: 45-50, 2002). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 49.

Annexin

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We found that annexin 1 (Seq ID No. 51) and annexin 2 (Seq ID No. 19) have high level of expression in PC. Both are members of a family of Ca^{2+}-dependent membrane-binding proteins. Described functions include, among others, an important role in malignant transformation (Masaki, T., et al., Hepatology, 24: 72-81, 1996), the control of epithelial cell line proliferation (Solito, E., et al., Cell Growth Differ., 9: 327-336, 1998), and mediation of apoptosis (Canaider, S., et al., Life Sci., 66: L265-L270, 2000). Evidence in support of causative roles for any annexins in the development of cancer is still mainly circumstantial. In MCF-7 breast carcinoma cells, overexpression of annexin1 led to abrogation of Ca2+ release after activation of purinergic or bradykinin receptors (Frey, B. M., et al., FASEB J., 13: 2235-2245, 1999), while over expression of annexin1 in rat 2 fibroblasts leads to direct inhibition of cytosolic PLA2, which in turn depresses the serum response element of c-fos (Oh, J., et al., FEBS Lett., 477: 244-248, 2000). Collectively, these studies imply a growth-suppressive role for annexin1. These results are not supported by the finding that annexin 1 is strongly up-regulated in a prostate cancer cell line (Vaarala, M. H., Lab Invest, 80: 1259-1268, 2000), esophageal cancer (Emmert-Buck, M. R., et al.,Mol.Carcinog., 27: 158-165, 2000), a stomach cancer cell line (Sinha, P., et al.,J.Biochem.Biophys.Methods, 37: 105-116, 1998), mammary adenocarcinoma (Pencil, S. D. and Toth, M. Clin.Exp.Metastasis, 16: 113-121, 1998), and hepatocarcinoma (de Coupade, C., et al., Hepatology, 31: 371-380, 2000). In hepatocarcinoma, study also showed that the proliferative rate of both normal and malignant hepatocytes was attenuated by antisense to annexin 1. These and our data suggest that cell growth is associated with elevated rather than reduced levels of annexin 1, which is also supported by the studies of Iacobuzio- Donahue et al. (Am. J. Pathol., 160: 1239-1249, 2002). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 51. In another preferred embodiment, the marker comprises Seq. ID No. 19.

Some additional proteins highly expressed in PC may have either clear roles in PC or an indirect link with PC, e.g. BGH3 (TGF-β1-induced protein, Seq ID No. 6) which is a secretory protein and acts as a marker for biologically active TGF-β 1 (Langham, R. G., et al., Transplantation, 72: 1826-1829, 2001). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 6.

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With the identification of polypeptides regulated in pancreatic cancer, the present invention provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of obtaining a biological sample; and detecting and/or measuring the increase of a marker described hereinbefore. The term "detection" as used herein refers to the qualitative determination of the absence or presence of polypeptides. The term "measured" as used herein refers to the quantitative determination of the differences in expression of polypeptides in biological samples from patients with pancreatic cancer and biological samples from healthy individuals. Methods for detection and/or measurement of polypeptides in biological samples are well known in the art and include, but are not limited to, Western-blotting, ELISAs or RIAs . Antibodies recognizing the polypeptides listed in table 2, 3, 5 and/or 6 can either be generated for the purpose of detecting said polypeptides, eg. by immunizing rabbits with purified proteins, or known antibodies recognizing said polypeptides can be used. For example, an antibody capable of binding to the denatured proteins, such as a polyclonal antibody, can be used to detect the peptides of this invention in a Western Blot. An example for a method to measure a marker is an ELISA. This type of protein quantitation is based on an antibody capable of capturing a specific antigen, and a second antibody capable of detecting the captured antigen. A further method for the detection of a diagnostic marker for pancreatic cancer is by analysing biopsy specimens for the presence or absence of the markers of this invention. Methods for the detection of these markers are well known in the art and include, but are not limited to, immunohistochemistry or immunofluorescent detection of the presence or absence of the polypeptides of the marker of this invention. Methods for preparation and use of antibodies, and the assays mentioned hereinbefore are described in Harlow, E. and Lane, D. Antibodies: A Laboratory Manual, (1988), Cold Spring Harbor Laboratory Press.

The accuracy of the diagnosis of pancreatic cancer can be increased by analysing combinations of multiple polypeptides listed in tables table 2, 3, 5 and/or 6. Thus, the in vitro method herein before described, comprises a marker which comprises at least two, preferably at least three, more preferably at least four, even more preferably at least five, and most preferably at least six of the polypeptides listed in table 2,3, 5 and/or 6.

For diagnosis of pancreatic cancer, suitable biological samples need to be analysed for the presence or absence of a marker. Said biological samples can be serum, plasma,

pancreatic juice or cells of pancreatic tissue. Cells from pancreatic tissue can be obtained by ERCP, secretin stimulation, fine-needle aspiration, cytologic brushings and large-bore needle biopsy.

It is also possible to diagnose pancreatic cancer by detecting and/or measuring nucleic acid molecules coding for the marker hereinbefore described. Preferably, said nucleic acid molecule is RNA or DNA. In another embodiment, said DNA is a cDNA.

In one embodiment of the present invention, the in vitro method herein before described comprises comparing the expression levels of at least two of the nucleic acids encoding said polypeptides in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer, to the expression levels of the same nucleic acids in a healthy individual.

In another embodiment of the present invention the in vitro method herein before described comprises comparing the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer to the expression levels of the same marker in a healthy individual. In a more preferred embodiment of the in vitro method, an increase or decrease of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

The present invention also provides a screening method for identifying and/or obtaining a compound which interacts with a polypeptide listed in table 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and detecting the interaction between said compound or plurality of compounds with said polypeptide.

The "interaction" in the screening methods as disclosed herein may be measured by conventional methods. The type of conventional method for testing the interaction of a

compound with a polypeptide that is soluble, as opposed to membrane associated, can be an in vitro method using either purified recombinant polypeptide, or native polypeptide purified from cells that endogenously express the polypeptide. As a non-limiting example, a polypeptide of the invention can be bound to beads or immobilized on plastic or other surfaces, and interaction of a compound with the polypeptide can be measured by either using a labelled compound and measuring the label bound to the polypeptide or by displacement of a labeled known ligand from said polypeptide.

For polypeptides that are associated with the cell membrane on the cell surface, or which are expressed as transmembrane or integral membrane polypeptides, the interaction of a compound with said polypeptides can be detected with different methods which include, but are not limited to, methods using cells that either normally express the polypeptide or in which the polypeptide is overexpressed, eg. by detecting displacement of a known ligand which is labeled by the compound to be screened. Alternatively, membrane preparations may be used to test for interaction of a compound with such a polypeptide

Interaction assays to be employed in the method disclosed herein may comprise FRET-assays (fluorescence resonance energy transfer; as described, inter alia, in Ng, Science 283 (1999), 2085-2089 or Ubarretxena-Belandia, Biochem. 38 (1999), 7398-7405), TR-FRETs and biochemical assays as disclosed herein. Furthermore, commercial assays like "Amplified Luminescent Proximity Homogenous Assay"™» (BioSignal Packard) may be employed. Further methods are well known in the art and, inter alia, described in Fernandez, Curr. Opin. Chem. Biol. 2 (1998), 547-603.

The "test for interaction" may also be carried out by specific immunological and/or biochemical assays which are well known in the art and which comprise, e.g., homogenous and heterogenous assays as described herein below. Said interaction assays employing read-out systems are well known in the art and comprise, inter alia, two-hybrid screenings (as, described, inter alia, in EP-0 963 376, WO 98/25947, WO 00/02911; and as exemplified in the appended examples), GST-pull-down columns, co-precipitation assays from cell extracts as described, inter alia, in Kasus-Jacobi, Oncogene 19 (2000), 2052-2059, "interaction-trap" systems (as described, inter alia, in US

6,004,746) expression cloning (e.g. lamda gt11), phage display (as described, inter alia, in US 5,541,109), in vitro binding assays and the like. Further interaction assay methods and corresponding read out systems are, inter alia, described in US 5,525,490, WO 99/51741, WO 00/17221, WO 00/14271 or WO 00/05410. Vidal and Legrain (1999) in Nucleic Acids Research 27, 919-929 describe, review and summarize further interaction assays known in the art which may be employed in accordance with the present invention.

Homogeneous (interaction) assays comprise assays wherein the binding partners remain in solution and comprise assays, like agglutination assays. Heterogeneous assays comprise assays like, inter alia, immuno assays, for example, Enzyme Linked Immunosorbent Assays (ELISA), Radioactive Immunoassays (RIA), Immuno Radiometric Assays (IRMA), Flow Injection Analysis (FIA), Flow Activated Cell Sorting (FACS), Chemiluminescent Immuno Assays (CLIA) or Electrogenerated Chemiluminescent (ECL) reporting.

The present invention further provides a screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of a) contacting said polypeptide with a compound identified and/or obtained by the screening method described above under conditions which allow interaction of said compound with said polypeptide; b) determining the activity of said polypeptide; c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist. The terms inhibitors and antagonists as used herein are used interchangeably. This screening assay can be performed either as an in vitro assay, or as a host-based assay. The host to be employed in the screening methods of the present invention and comprising and/or expressing a polypeptide listed in table 2, 3, 5 and/or 6 may comprise prokaryotic as well as eukaryotic cells. Said cells may comprise bacterial cells, yeast cells, as well as cultured (tissue) cell lines, inter alia, derived from mammals. Furthermore animals may also be employed as hosts, for example an non-human transgenic animal. Accordingly, said host (cell) may be transfected or transformed with the vector comprising a nucleic acid molecule coding for a polypeptide which is differentially regulated in pancreatic cancer as disclosed herein. Said host cell or host may therefore be genetically modified with a nucleic acid molecule encoding such a

polypeptide or with a vector comprising such a nucleic acid molecule. The term "genetically modified" means that the host cell or host comprises in addition to its natural genome a nucleic acid molecule or vector coding for a polypeptide listed in table 2, 3, 5 and/or 6 or at least a fragment therof. Said additional genetic material may be introduced into the host (cell) or into one of its predecessors/parents. The nucleic acid molecule or vector may be present in the genetically modified host cell or host either as an independent molecule outside the genome, preferably as a molecule which is capable of replication, or it may be stably integrated into the genome of the host cell or host.

As mentioned herein above, the host cell of the present invention may be any prokaryotic or eukaryotic cell. Suitable prokaryotic cells are those generally used for cloning like E. coli or Bacillus subtilis. Yet, these prokaryotic host cells are also envisaged in the screening methods disclosed herein. Furthermore, eukaryotic cells comprise, for example, fungal or animal cells. Examples for suitable fungal cells are yeast cells, preferably those of the genus Saccharomyces and most preferably those of the species Saccharomyces cerevisiae. Suitable animal cells are, for instance, insect cells, vertebrate cells, preferably mammalian cells, such as e.g. CHO, HeLa, NIH3T3 or MOLT-4. Further suitable cell lines known in the art are obtainable from cell line depositories, like the American Type Culture Collection (ATCC).

The hosts may also be selected from non-human mammals, most preferably mice, rats, sheep, calves, dogs, monkeys or apes. As described herein above, said animals/mammals also comprise non-human transgenic animals, which preferably express at least one polypeptide differentially regulated in pancreatic cancer as disclosed herein. Preferably, said polypeptide is a polypeptide which is up-regulated in tissue derived from patients with pancreatic cancer. Yet it is also envisaged that non-human transgenic animals be produced which do not express marker genes as disclosed herein or who express limited amounts of said marker gene products. Said animals are preferably related to polypeptides which are down-regulated in pancreatic cancer. Transgenic non-human animals comprising and/or expressing the up-regulated polypeptides of the present invention or alternatively, which comprise silenced or less efficient versions of down-regulated polypeptides are useful models for studying the development of pancreatic cancer and provide for useful models for testing drugs and therapeutics for pancreatic cancer treatment and/or prevention.

A compound which interacts with a polypeptide listed in table 2, 3, 5 and/or 6 and which inhibits or antagonizes said polypeptide is identified by determining the activity of said polypeptide in the presence of said compound.

The term "activity" as used herein relates to the functional property or properties of a specific polypeptide. For the enzymes listed in table 2, 3, 5 and/or 6, the term "activity" relates to the enzymatic activity of a specific polypeptide. Activity assays for the enzymes listed in table 2, 3, 5 and/or 6 are well known.

For adhesion molecules listed in table 2, 3, 5 and/or 6, the term "activity" relates to the adhesive properties of a polypeptide and may determined using assays such as, but not limited to, adhesion assays, cell spreading assays, or in vitro interaction of the adhesion molecule with a known ligand. Such assays are well known in the art.

For cytoskeletal proteins, the term "activity" relates to the regulation of the cytoskeleton by such polypeptides, or to their incorporation into the cytoskeleton. As a non-limiting example, the ability of Gelsolin to regulate actin polymerization, or of Filamin A to promote orthogonal branching of actin filaments, may be determined using in vitro actin polymerization assays. Activity in relation to the regulation of cytoskeletal structures may further be determined by, as non-limiting examples, cell spreading assays, cell migration assays, cell proliferation assays or immunofluorecence assays, or by staining actin filaments with fluorescently labeled phalloidin. All of these assays are well known to the person skilled in the art.

For ion channels (Chloride intracellular channel protein) the term "activity" relates to ion flux (Chloride lux) across the membrane. Methods to determine ion flux across membranes are well known to the person skilled in the art.

For transcription factors, eg. KIAA 1034, the term "activity" relates to their ability to regulate gene transcription. The transcriptional activity of a polypeptide can be determined using commonly used assays, such as a reporter gene assay.

For growth factors and hormones or their receptors, the term "activity" relates to their ability to bind to their receptors or ligands, respectively, and to induce receptor activation and subsequent signaling cascades, and/or it relates to the factor's or receptor's ability to mediate the cellular function or functions eventually caused by growth factor or hormone mediated receptor activation. Growth factor or hormone binding to receptors can be determined by commonly known ligand binding assays. Receptor activation can be determined by testing for receptor auto-phosphorylation, or by assaying for modification or recruitment of downstream signaling mediators to the receptors (by immunoprecipitation and Western Blotting of signaling complexes). Cellular functions regulated by growth factors or hormones and their receptors can be cell proliferation (eg determined by using thymidine incorporation or cell counts), cell migration assays (eg determined by using modified Boyden chambers), cell survival or apoptosis assays (eg determined by using DAPI staining), angiogenesis assays (eg in vitro assays to measure endothelial tube formation that are commercially available). In addition to these assays, other assays may be used as well to determine these and other cellular functions.

Inhibitors or antagonists of a polypeptide listed in tables 2 and/or 3 are identified by the screening method described above when there is a decreased activity determined in the presence of the compound in comparison to the absence of the compound in the screening method, which is indicative for an inhibitor or antagonist.

Further to the screening methods disclosed above, this invention provides a screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of a) contacting a host which expresses said polypeptide with a compound; b) determining the expression level and/or activity of said polypeptide; c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and d) quantitatively relating the expression level of said polypeptide as determined in (b) and

(c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

An inhibitor of the expression of a polypeptide listed in table 2, 3, 5 and/or 6 is identified by the screening method described hereinbefore when a decreased expression of the protein is determined in the presence of the compound in comparison to the absence of the compound in the screening method, which is indicative for an inhibitor of expression of a polypeptide.

The term "express" as used herein relates to expression levels of a polypeptide listed table 2, 3, 5 and/or 6 which is up-regulated in pancreatic cancer, in cells, preferably in a pancreatic adenocarcinoma cell line, which are elevated as compared to the expression levels of the same polypeptide in healthy pancreatic cells. Preferably, expression levels are at least 2 fold, more preferably at least 3 fold, even more preferably at least 4 fold, most preferably at least 5 fold higher than in healthy pancreatic cells.

Furthermore, the present invention provides a compound identified and/or obtained by any of the screening methods hereinbefore described. Said compound is further comprised in a pharmaceutical composition. A method for the preparation of said pharmaceutical composition comprising formulating said compound in a pharmaceutically acceptable carrier or diluent is also claimed. Any conventional carrier material can be utilized. The carrier material can be an organic or inorganic one suitable for eteral, percutaneous or parenteral administration. Suitable carriers include water, gelatin, gum arabic, lactose, starch, magnesium stearate, talc, vegetable oils, polyalkylene-glycols, petroleum jelly and the like. Furthermore, the pharmaceutical preparations may contain other pharmaceutically active agents. Additional additives such as favoring agents, stabilizers, emulsifying agents, buffers and the like may be added in accordance with accepted practices of pharmaceutical compounding.

Said compound may be used for the preparation of a medicament for the treatment or prevention of pancreatic cancer. In addition, said compound may also be used for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer. Preferably, said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

Within the scope of the present invention, antibodies against the proteins listed in tables 2 and/or 3, or antigen-binding fragments thereof, may be used in an in vitro method for the diagnosis of pancreatic cancer.

In order to efficiently perform diagnostic screenings, the present invention provides a kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, described above. Another kit provided by this invention is a kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker hereinbefore described. Yet another kit provided by this invention is a kit for screening of compounds that antagonize any of the polypeptides listed in tables 2 and/or 3 or inhibit the expression of any of said polypeptides.

The present invention pertains to a marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 6. Preferably, said marker does not include Seq ID No.s 25 and 50 to 55. In a more preferred embodiment, said marker comprises at least one of the polypeptides listed in table 5.

The present invention also provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

a) obtaining a biological sample; and

b) detecting and/or measuring the increase of at least one of the polypeptides listed in table 6.

Preferably, said in vitro method additionally comprises the step of detecting and/or measuring the decrease of at least one of the polypeptides listed in table 5. More preferably, in said vitro method, said at least one polypeptide does not include Seq ID No.s 25 and 50 to 55. Even more preferably, in said vitro method, said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.

The present invention further provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

a) obtaining a biological sample; and

b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker hereinbefore described.

Preferably, in said in vitro method, said nucleic acid molecule is RNA or DNA. More preferably, in said in vitro method, said DNA is a cDNA.

In a further more preferred embodiment of any of the in vitro methods hereinbefore described, the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual. In a most preferred embodiment of any of the in vitro methods hereinbefore described, the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.

In a further preferred embodiment of the in vitro method hereinbefore described, an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

The present invention also pertains to a screening method for identifying and/or obtaining a compound which interacts with a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

Furthermore, the present invention provides a screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound identified and/or obtained by the screening method of claim 39 under conditions which allow interaction of said compound with said polypeptide;

b) determining the activity of said polypeptide;

c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.

The present invention also provides a screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting a host which expresses said polypeptide with a compound,

b) determining the expression level and/or activity of said polypeptide;

c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

The present invention provides a compound identified and/or obtained by the screening methods hereinbefore described.

In addition, the present invention provides a pharmaceutical composition comprising the compound hereinbefore described. Also provided is a method for the preparation of the pharmaceutical composition hereinbefore described comprising formulating the compound hereinbefore described in a pharmaceutically acceptable carrier or diluent.

The present invention provides a use of a compound hereinbefore described for the preparation of a medicament for the treatment or prevention of pancreatic cancer.

Also provided is a use of a compound hereinbefore described for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer. In a preferred embodiment, the uses hereinbefore described relate to a compound comprising an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

Within the scope of the present invention, antibodies against the proteins listed in tables 5 and/or 6, or antigen-binding fragments thereof, may be used in an in vitro method for the diagnosis of pancreatic cancer.

In order to efficiently perform diagnostic screenings, the present invention provides a kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, described above. Another kit provided by this invention is a kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker hereinbefore described. Yet another kit provided by this invention is a kit for screening of compounds that antagonize any of the polypeptides listed in tables 5 and/or 6 or inhibit the expression of any of said polypeptides.

In the present invention, the proteins, compounds, kits, methods and uses substantially as herein before described, especially with reference to the foregoing examples are also claimed.

Examples:

Collection of tissue samples

5 Pancreatic carcinomas and adjacent tissue were collected from the patients listed in table 1.

Samples were collected shortly after the resection (less than 30 minutes), and fast frozen in liquid nitrogen for about 1 minute, then stored in a freezer at a temperature of –80°C.

10 Characterization of formalin-fixed specimens

Histopathological characterization was carried out by using hematoxylin-eosin-stained sections of formalin-fixed and paraffin-embedded specimens. Tumors were classified using the WHO system. The types of pancreatic carcinomas included in the study are shown in table 1.

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The twelve pancreatic carcinoma samples used in this study were ductal carcinomas which constitute the overwhelming proportion of pancreatic carcinomas. The patient-matched samples from histologically normal tissue surrounding the carcinoma were used as controls. We carried out 12 pairs of 2-dimensional electrophoresis maps for
20 comparing protein expression between tumor tissue and normal control tissue. For protein identification, the samples were pooled, thus generating pan-Carcinoma and pan-Normal protein extracts. Quantification was carried out in two steps: (I) Gels from the pooled samples were compared using the PDQuest image analysis software. (II) The changes identified at the level of the pooled samples were cross-validated by an analysis of
25 the individual samples. The change factors shown in table 2, 3, 5 and 6 were determined using the pooled samples.

Preparation of samples for electrophoresis

Samples cleaned of clots and contaminating tissue were frozen in liquid nitrogen, then ground to powder. Samples were suspended in lysis buffer (8M urea, 4% CHAPS, 40mMol/L Tris-Cl, 0.5% carrier ampholytes, 100mMol/L DTT and 0.1lg/ll PMSF) and centrifuged at 12000rpm for 30 minutes. The supernatants were stored at –80°C. The protein concentration in the extracts was determined by the Bradford method (Bradford, M. Anal. Biochem. 72, 248 (1976).

Two-dimensional gel electrophoresis

Samples containing 1 mg of protein were loaded onto the rehydrated IPG strip (18 cm, pH3~10) by using the cup loading method. IEF was performed using Pharmacia Multiphor apparatuses under the following conditions: First, the voltage was increased 200V-5000V over 24hrs, then a constant voltage of 5000V was applied for 24 hrs, the running temperature was 20°C. After IEF, the strips were equilibrated with 10 ml equilibration solution I (6 M Urea, 50 mM Tris pH 8.8, 30 % Glycerol, 2.0 % SDS, 30 mM Dithioerythritol) for 15 min, then for another 15 min with equilibration solution II (6 M Urea, 50 mM Tris pH 8.8, 30 % Glycerol, 2.0 % SDS, 0.23 M Iodoacetamide).

The second dimension SDS polyacrylamide gel electrophoresis (SDS-PAGE) was carried out using a Hoefer ISO_DALT apparatus (10 gels/run, 24x20 cm), IEF strips were loaded onto 12% homogeneous polyacrylamide gels (1.5 mm x 24 cm x 20 cm). The gels were run in TGS_Buffer (250 mM Tris, 1.92 M Glycine, 1% (w/v) SDS, pH = 8.3, Bio-Rad) at a constant voltage (80 V, 20°C).

Gel fixation and staining

Gels were fixed in 50% Methanol/20% acetic acid for 30 min, then washed in ultra-pure water for 30 min and stained with NOVEX Colloidal Blue staining Kit (Invitrogen) following the manufacturer's recommendations.

Protein Identification

The protein identification was performed using a two-step procedure.

In-gel digestion

Spots were picked and transferred into 96-well by a spot picking robot. From each gel, 600-800 spots were picked. The spots were destained with 100µl of 30% acentonitrile in 50Mm ammonium bicarbonate, washed in ultra pure-water and dried in a speed vac evaporator. The dry gel pieces were digested with 10ng/µl trypsin (Promega, Madison, USA) solution in 500 nM ammonium bicarbonate at room temperature for 16 h maximum. The peptides from each spot were extracted with 20µl of 0.1% trifluoro acetic acid (TFA) in 50% acetonitrile. The matrix solution consisted of 0.025%(w/v) alfa-cyano-4-hydroxy cinammic acid (Sigma) in 50% acetonitrile/0.1% TFA with internal standard peptides des-Arg-Bradykinin(Sigma, MW 904.4681 Da) and adrenocorticotropic hormone fragment 18-39 (Sigma, MW 2465.1989 Da).

Analysis by MALDI-TOF

1.5ul of peptide extract and 1.0µl of matrix solution were stimulaneously applied to the spots on the MS target. Recrytallization was carried out as specified by the instruments manufacturer. The samples were analyzed in a MALDI-time of flight Mass spectrometer (Autoflex, Bruker Analytics, Bremen, Germany). Peak annotation and database search by peptide matching was performed by in house developed software. The peptide mass was compared with theoretic peptide masses of all available proteins from all species. The monoisotopic mass was used and a mass tolerence of 0.002% was allowed. 4 matching peptides were the minimal requirement for an identity assigment. Mismatch or miscleavage sites were not considered.

Table 2: Proteins up-regulated in pancreatic cancer I

Protein	Acc No	Description	Seq ID No.	Fold Change
sw:CATD_HUMAN	P07339	Cathepsin D precursor (ec 3.4.23.5).	1	<2
sw:IDHC_HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic (ec 1.1.1.42)	2	2
sw:GELS_HUMAN	P06396	Gelsolin precursor, plasma	3	3
sw:CFAB_HUMAN	P00751	Complement factor B precursor (ec 3.4.21.47)	4	5
sw:AAC4_HUMAN	O43707	Alpha-actinin 4 (non-muscle alpha-actinin 4)	5	2
sw:AAC1_HUMAN	P12814	Alpha-actinin 1 (alpha-actinin cytoskeletal isoform)	7	2
sw:TBA4_HUMAN	P05215	Tubulin alpha-4 chain.	8	2
sw:ABP2_HUMAN	P21333	Filamin A (Endothelial actin-binding protein)	9	4
sw:TAGL_HUMAN	P37802	Transgelin 2 (smooth muscle protein 22-alpha)	10	2
sw:TPM4_HUMAN	P07226	Tropomyosin alpha 4 chain	11	<2
sw:BGH3_HUMAN	Q15582	Transforming growth factor-beta induced protein IG-H3 precursor	6	5
sw:CALD_HUMAN	Q05682	Caldesmon (cdm)	12	2
sw:ENOL_HUMAN	Q05524	Alpha enolase	13	2
sw:ACY1_HUMAN	Q03154	Aminoacylase-1	14	5
sw:CAPB_HUMAN	P47756	F-actin capping protein beta subunit (capz beta)	15	5
sw:IPYR_HUMAN	Q15181	Inorganic pyrophosphatase	16	<2
sw:LEG3_HUMAN	P17931	Galectin-3 (galactose-specific lectin 3).	17	2

Table 1: Clinical and histopathological characteristics of samples

No. of Samples	Sex	Age	Tumor location	Histology	Metastasis in lymph nodes
PC-01	Male	48	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-02	Male	68	Head of pancreas	Poorly differentiated adenocarcinoma	Yes
PC-03	Male	44	Head of pancreas	Poorly differentiated ductal adenocarcinoma, clear cell type	Yes
PC-04	Male	66	Head of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-05	Female	45	Head of pancreas	Well differentiated ductal adenocarcinoma	No
PC-06	Female	65	Head of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-07	Male	59	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-08	Female	62	Body of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-09	Male	54	Head of pancreas	Middle differentiated ductal adenocarcinoma	No
PC-10	Female	53	Head of pancreas	Well differentiated ductal adenocarcinoma	No
PC-11	Female	54	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-12	Female	69	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes

sw:MLEN_HUMAN	P16475	Myosin light chain alkali, non-muscle isoform	39	3
sw:CALX_HUMAN	P27824	Calnexin precursor	40	3
sw:MA32_HUMAN	Q07021	Complement component 1	41	<2
sw:NUAM_HUMAN	P28331	NADH-ubiquinone oxidoreductase 75 kda subunit, mitochondrial precursor	42	2
sw:PBEF_HUMAN	P43490	Pre-B cell enhancing factor precursor.	43	2
sw:RETL_HUMAN	P09455	Retinol-binding protein I, cellular	44	2
sw:TCPG_HUMAN	P49368	T-complex protein 1, gamma subunit	45	2
sw:RINI_HUMAN	P13489	Placental ribonuclease inhibitor	46	<2
sw:GBLP_HUMAN	P25388	Guanine nucleotide-binding protein beta subunit-like protein 12.3	47	2
sw:S109_HUMAN	P06702	Calgranulin B	49	<2

sw:POR2_HUMAN	P45880	Voltage-dependent anion-selective channel protein 2	18	<2
SW:ANX2_HUMAN	P07355	Annexin II	19	2
sw:CBP2_HUMAN	P50454	Collagen-binding protein 2 precursor	20	2
sw:COFI_HUMAN	P23528	Cofilin, non-muscle isoform	21	<2
sw:CYPH_HUMAN	P05092	Peptidyl-prolyl cis-trans isomerase A	22	<2
sw:DYI2_HUMAN	Q13409	Dynein intermediate chain 2, cytosolic	23	2
sw:ECH1_HUMAN	Q13011	Delta3,5-Delta2,4-dienoyl-coa isomerase, mitochondrial precursor	24	2
sw:MLRN_HUMAN	P24844	Myosin regulatory light chain 2	48	2
sw:PLSL_HUMAN	P13796	L-Plastin	26	<2
sw:RAN_HUMAN	P17080	GTP-binding nuclear protein ran	27	3
sw:ROK_HUMAN	Q07244	Heterogeneous nuclear ribonucleoprotein k	28	2
sw:TCTP_HUMAN	P13693	Translationally controlled tumor	29	<2
sw:TPM1_HUMAN	P09493	Tropomyosin 1 alpha chain	30	<2
sw:TYPH_HUMAN	P19971	Thymidine phosphorylase precursor	31	5
sw:AMPL_HUMAN	P28838	Cytosol aminopeptidase	32	3
sw:KICS_HUMAN	P08727	Keratin, type i cytoskeletal 19 (cytokeratin 19)	33	4
sw:ALDX_HUMAN	P14550	Alcohol dehydrogenase [NADP+]	34	4
sw:EL3A_HUMAN	P09093	Elastase IIIa precursor	35	4
sw:DLDH_HUMAN	P09622	Dihydrolipoamide dehydrogenase, mitochondrial precursor	36	2
sw:ECHM_HUMAN	P30084	Enoyl-CoA hydratase, mitochondrial precursor	37	3
sw:HSBX_HUMAN	O14558	Heat-shock 20 kDa like-protein p20.	38	2

Table 4. Proteins roughly classified by their involved biological processing or basic function

Protein function[a]	Number[b]	Percentage (%)[c]
Structural constitural and regulation of cytoskeleton	61	20.8
Cell cycle and metabolism	74	25.3
Response to external stimulus or stress	61	20.8
Signal transduction	13	4.4
Nuclear function	18	6.1
Transport processing	19	6.5
Hemostatis	12	4.1
Cell adhension	7	2.4
Chaperon	7	2.4
Apoptosis	3	1
Unknown function	11	3.7
Others	7	2.4
Total	293	100

Table 3: Proteins up-regulated in pancreatic cancer II

Protein	Acc No	Description	Seq ID No	Fold Change
sw:CAPG_HUMAN	P40121	Macrophage capping protein	50	3
sw:ANX1_HUMAN	P04083	Annexin I (lipocortin I) (calpactin II)	51	4
sw:K2C7_HUMAN	P08729	Keratin, type II cytoskeletal 7	52	5
humangp:CHR13-Q15063	Q15063	Osteoblast specific factor 2 precursor	53	2
sw:TGLC_HUMAN	P21980	Protein-glutamine gamma-glutamyltransferase	54	2
sw:GDIR_HUMAN	P52565	Rho GDP-dissociation inhibitor 1	55	<2
sw:IQG1_HUMAN	P46940	Ras GTPase-activating-like protein	25	2

5

Table 5. Proteins with higher levels in normal pancreatic compared to cancer tissue

Protein[a]	AccNo[b]	Description[c]	Fold[d]	Seq ID No.
cytoskeletal regulation				
sw:DESM_HUMAN	P17661	desmin.	3	70
proteolysis and peptidolysis				
sw:CBPB_HUMAN	P15086	carboxypeptidase b precursor	2	71
sw:CBP1_HUMAN	P15085	carboxypeptidase a1 precursor	Uncalculated	72
sw:CPB2_HUMAN	P50454	carboxypeptidase a2 precursor	Uncalculated	73
sw:CTRB_HUMAN	P17538	chymotrypsinogen b precursor	Uncalculated	74
sw:TRY1_HUMAN	P07477	trypsin i precursor (ec 3.4.21.4) (cationic trypsinogen).	Uncalculated	75
sw:TRY2_HUMAN	P07478	trypsin ii precursor (anionic trypsinogen).	3	76
sw:ILEU_HUMAN	P30740	leukocyte elastase inhibitor	4	77
chaperon				
sw:CH60_HUMAN	P10809	human. mitochondrial matrix protein p1 precursor	2	78
sw:ENPL_HUMAN	P14625	94 kda glucose-regulated protein	3	79
SW:ER29_HUMAN	P30040	endoplasmic reticulum protein erp29 precursor	2	80
sw:PDA2_HUMAN	Q13087	protein disulfide isomerase a2 precursor	2	81
sw:PDA3_HUMAN	P30101	protein disulfide isomerase a3 precursor	2	82
oxidoreductase				
sw:ADHB_HUMAN	P00325	alcohol dehydrogenase beta chain	<2	83
sw:GTO1_HUMAN	P78417	glutathione transferase omega 1	Uncalculated	84
sw:OXRP_HUMAN	Q9Y4L1	150 kda oxygen-regulated protein precursor	Uncalculated	85
sw:PDX4_HUMAN	Q13162	peroxiredoxin 4	<2	86
sw:ULA4_HUMAN	P30039	mawd binding protein	<2	87
metabolism of biological process				
sw:AMYC_HUMAN	P19961	alpha-amylase 2b precursor	3	88
sw:AMYP_HUMAN	P04746	alpha-amylase, pancreatic precursor	Uncalculated	89
sw:ATPA_HUMAN	P25705	atp synthase alpha chain, mitochondrial precursor	<2	90
sw:BAL_HUMAN	P19835	bile-salt-activated lipase precursor	3	91
sw:LIP1_HUMAN	P54315	pancreatic lipase related protein 1 precursor .	<2	92
sw:LIP2_HUMAN	P54317	pancreatic lipase related protein 2 precursor	Uncalculated	93
sw:LIPP_HUMAN	P16233	triacylglycerol lipase, pancreatic precursor	Uncalculated	94
sw:DPY2_HUMAN	Q16555	dihydropyrimidinase related protein-2		95
sw:GABT_HUMAN	P80404	4-aminobutyrate aminotransferase	2	96
sw:GATM_HUMAN	P50440	glycine amidinotransferase, mitochondrial precursor	Uncalculated	97
sw:GR78_HUMAN	P11021	78 kda glucose-regulated protein precursor (grp 78)	3	98
sw:IF32_HUMAN	Q13347	eukaryotic translation initiation factor 3 subunit 2	<2	99
sw:DPY2_HUMAN	Q16555	dihydropyrimidinase related protein-2		100
sw:PGMU_HUMAN	P36871	phosphoglucomutase	2	101
sw:PSA1_HUMAN	P25786	proteasome subunit alpha type 1	2	102
heat shock protein				
sw:HS27_HUMAN	P04792	heat shock 27 kda protein	Uncalculated	103
signaling				
SW:PD61	Q8WUM4	programmed cell death 6 interacting protein	5	104
muscle development				

Table 6 Proteins with higher levels in pancreatic cancer compared to in normal tissue

Protein [a]	AccNo [b]	Description [c]	Fold [d]	Seq ID No.
cytoskeletal regulation				
sw:FSC2_HUMAN	O14926	fascin 2 (retinal fascin).	2	56
sw:AAC1_HUMAN	P12814	alpha-actinin 1	2	7
sw:AAC4_HUMAN	O43707	alpha-actinin 4	2	5
sw:ABP2_HUMAN	P21333	endothelial actin-binding protein (alpha-filamin).	4	9
sw:ANX2_HUMAN	P07355	human annexin ii (lipocortin ii)	2	19
sw:CALD_HUMAN	Q05682	caldesmon (cdm).	2	12
sw:CAPB_HUMAN	P47756	f-actin capping protein beta subunit	5	15
sw:CAPG_HUMAN	P40121	macrophage capping protein	3	50
sw:COF1_HUMAN	P23528	cofilin, non-muscle isoform (p18).	<2	21
sw:DEST_HUMAN	P18282	destrin (actin-depolymerizing factor) (adf).	2	57
sw:DYI2_HUMAN	Q13409	dynein intermediate chain 2(fragment).	2	23
sw:GELS_HUMAN	P06396	gelsolin precursor	3	3
sw:KICS_HUMAN	P08727	keratin, type i cytoskeletal 19	4	33
sw:K2C7_HUMAN	P08729	keratin, type ii cytoskeletal 7	5	52
sw:MLEN_HUMAN	P16475	myosin light chain alkali	3	39
sw:PLSL_HUMAN	P13796	l-plastin (lymphocyte cytosolic protein 1)	<2	26
sw:TAGL_HUMAN	P37802	transgelin (22 kda actin-binding protein).	2	10
sw:TBA4_HUMAN	P05215	tubulin alpha-4 chain.	2	8
proteolysis and peptidolysis				
sw:ACY1_HUMAN	Q03154	aminoacylase-1	5	14
sw:AMP1_HUMAN	P28838	cytosol aminopeptidase	3	32
sw:CATD_HUMAN	P07339	cathepsin d precursor.	<2	1

h:aup:057687-10-0	Q9bva2	four and a half lim domains 3	<2	105
SW:sli2	Q13643	Skeletal muscle LIM-protein 2 (SLIM 2)(Four and a half LIM domains protein 3)(FHL3).	<2	106
transport of biological process				
sw:CYB5_HUMAN	P00167	cytochrome b5.	2	107
cell adhesion				
sw:PAP1_HUMAN	Q06141	pancreatitis-associated protein 1 precursor.	Uncalculated	108
other				
SW:CA16_HUMAN	P12109	collagen alpha 1(vi) chain precursor.	5	109
SW:LUM_HUMAN	P51884	lumican precursor	3	110

sw:CPAB_HUMAN	P00751	complement factor b precursor	5	4
sw:EL3A_HUMAN	P09093	elastase iiia precursor	4	35
chaperon				
sw:APE_HUMAN	P02649	apolipoprotein e precursor (apo-e).	<2	59
sw:CALX_HUMAN	P27824	calnexin precursor(p90)	3	40
sw:CYPH_HUMAN	P05092	peptidyl-prolyl cis-trans isomerase a	<2	22
sw:TCPG_HUMAN	P49368	t-complex protein 1, gamma subunit	2	45
sw:CBP2_HUMAN	P50454	human, collagen-binding protein 2 precurso	2	20
tr_hum:Q96C61	Q96C61	hypothetical 88.6 kda protein	5	60
oxidoreductase				
sw:DLDH_HUMAN	P09622	dihydrolipoamide dehydrogenase	2	36
sw:IDHC_HUMAN	O75874	isocitrate dehydrogenase [nadp] cytoplasmic	2	2
sw:NUAM_HUMAN	P28331	nadh-ubiquinone oxidoreductase 75 kda subunit	2	42
metabolism of biological process				
sw:ALDX_HUMAN	P14550	alcohol dehydrogenase [nadp+]	4	34
sw:ECH1_HUMAN	Q13011	delta3,5-delta2,4-dienoyl-coa isomerase	2	24
sw:ECHM_HUMAN	P30084	enoyl-coa hydratase, mitochondrial precursor	3	37
sw:IPYR_HUMAN	Q15181	inorganic pyrophosphatase	<2	16
sw:TYPH_HUMAN	P19971	thymidine phosphorylase precursor	5	31
SW:ENOA_HUMAN	P06733	human alpha enolase	2	61
sw:ENOL_HUMAN	Q05524	alpha enolase, lung specific	2	13
sw:SYW_HUMAN	P23381	tryptophanyl-trna synthetase	2	62
heat shock protein				
sw:HSBX_HUMAN	O14558	heat-shock 20 kda like-protein p20.	2	38
signaling				
sw:GBLP_HUMAN	P25388	guanine nucleotide-binding protein beta subunit-like protein 12.3	2	47

sw:GDIR_HUMAN	P52565	rho gdp-dissociation inhibitor 1	<2	55
sw:IQG1_HUMAN	P46940	ras gtpase-activating-like protein iqgap1	2	25
sw:PBBF_HUMAN	P43490	pre-b cell enhancing factor precursor.	2	43
sw:RAN_HUMAN	P17080	gtp-binding nuclear protein ran	3	27
immune response				
sw:KAC_HUMAN	P01834	ig kappa chain c region.	2	63
sw:MA32_HUMAN	Q07021	pre-mrna splicing factor sf2, p32 subunit.	<2	41
inflammatory reponse				
sw:ANXL_HUMAN	P04083	annexin i (lipocortin i)	4	51
sw:LEG3_HUMAN	P17931	galectin-3	2	17
sw:S109_HUMAN	P06702	calgranulin b (mrp-14)	<2	49
muscle development				
sw:TPM1_HUMAN	P09493	tropomyosin 1 alpha chain	<2	30
sw:TPM4_HUMAN	P07226	tropomyosin alpha 4 chain	<2	11
sw:MLRN_HUMAN	P24844	myosin regulatory light chain 2	2	48
transport of biological process				
humangp:CHR2-Q15092	Q15092	transmembrane protein.	2	64
sw:POR2_HUMAN	P45880	voltage-dependent anion-selective channel protein 2	<2	18
sw:RETL_HUMAN	P09455	retinol-binding protein l	2	44
RNA processing				
humangp:CHR20-Q9P2E9	O75300	ribosome binding protein 1 (kiaa1398 protein).	<2	65
sw:RINI_HUMAN	P13489	placental ribonuclease inhibitor	<2	46
sw:ROK_HUMAN	Q07244	heterogeneous nuclear ribonucleoprotein k	2	28
blood coagulation				
sw:FIBG_HUMAN	P02679	fibrinogen gamma chain precursor	3	66
sw:THRB_HUMAN	P00734	prothrombin precursor	<2	67
Anti-apoptosis				

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			<2	29
sw:TCTP_HUMAN	P13693	translationally controlled tumor protein (p23)		
cell adhesion				
humangp:CHR13-Q15063	Q15063	osteoblast specific factor 2 precursor	2	53
sw:BGH3_HUMAN	Q15582	transforming growth factor-beta induced protein	5	6
other				
sw:TGLC_HUMAN	P21980	tissue transglutaminase	2	54
sw:KPY1_HUMAN	P14618	Human pyruvate kinase, cytosolic thyroid hormone-binding protein	3	68
humangp:CHR19-Q96D15	Q96D15	Reticulocalbin 3 precursor.	2	69

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<u>Claims</u>

1. A marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in tables 2 and 3.

5   2. The marker of claim 1 wherein the group from which at least one polypeptide is selected consists of the polypeptides listed in table 2.

3. A polypeptide selected from the group consisting of the polypeptides listed in tables 2 and 3, for use as a marker or as a component of a marker for diagnosis of pancreatic
10 cancer and/or the susceptibility to pancreatic cancer.

4. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

a) obtaining a biological sample; and

15 b) detecting and/or measuring the increase of a marker of claims 1 or 2.

5. The in vitro method of claim 4, wherein the marker comprises at least two polypeptides.

20 6. The in vitro method of claims 4 or 5 wherein said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.

7. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

25 a) obtaining a biological sample; and

b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker of claims 1 or 2.

8.   The in vitro method of claim 7, wherein said nucleic acid molecule is RNA or DNA.

9.   The in vitro method of claim 8, wherein said DNA is a cDNA.

10.   The in vitro method of any one of claims 7 to 9, wherein the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual.

11.   The in vitro method of any one of claims 4 to 6, wherein the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.

12.   The in vitro method of claim 11, wherein an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

13.   A screening method for identifying and/or obtaining a compound which interacts with a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

14.   A screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting a said polypeptide with a compound identified and/or obtained by the screening method of claim 13 under conditions which allow interaction of said compound with said polypeptide;

b) determining the activity of said polypeptide;

c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.

15.   A screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting a host which expresses said polypeptide with a compound,

b) determining the expression level and/or activity of said polypeptide;

c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

16.   A compound identified and/or obtained by the screening methods of any one of claims 13 to 15.

17.   A pharmaceutical composition comprising the compound of claim 16.

18. A method for the preparation of the pharmaceutical composition of claim 17 comprising formulating the compound of claim 16 in a pharmaceutically acceptable carrier or diluent.

19. Use of a compound of claim 16 for the preparation of a medicament for the treatment or prevention of pancreatic cancer.

20. Use of a compound of claim 16 for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer.

21. The use of claim 19 or 20 wherein said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

22. Antibodies against the proteins listed in tables 2 and/or 3, or antigen-binding fragments thereof, for the use in an in vitro method for the diagnosis of pancreatic cancer.

23. A kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, of claim 22.

24. A kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker of claims 1 or 2.

25. A kit for screening of compounds that activate or inhibit any of the polypeptides listed in tables 2 and/or 3, or stimulate or inhibit the expression of any of said polypeptides.

26. A marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 6.

27. The marker of claim 26, wherein said at least one polypeptide does not include Seq ID No.s 25 and 50 to 55.

28. The marker according to any one of claims 26 to 27, additionally comprising at least one of the polypeptides listed in table 5.

29. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

a) obtaining a biological sample; and

b) detecting and/or measuring the increase of at least one of the polypeptides listed in table 6.

30. The in vitro method of claim 29, additionally comprising the step of detecting and/or measuring the decrease of at least one of the polypeptides listed in table 5.

31. The in vitro method of claims 29 or 30, wherein said at least one polypeptide does not include Seq ID No.s 25 and 50 to 55.

32. The in vitro method of any one of claims 29 to 31, wherein said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.

33. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

a) obtaining a biological sample; and

b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker of any one of claims 26 to 28.

34. The in vitro method of claim 33, wherein said nucleic acid molecule is RNA or DNA.

35. The in vitro method of claim 34, wherein said DNA is a cDNA.

36. The in vitro method of any one of claims 33 to 35, wherein the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual.

37. The in vitro method of any one of claims 33 to 36, wherein the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.

38. The in vitro method of claim 37, wherein an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

39. A screening method for identifying and/or obtaining a compound which interacts with a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

40. A screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound identified and/or obtained by the screening method of claim 39 under conditions which allow interaction of said compound with said polypeptide;

b) determining the activity of said polypeptide;

c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.

41. A screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting a host which expresses said polypeptide with a compound,

b) determining the expression level and/or activity of said polypeptide;

c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

42.   A compound identified and/or obtained by the screening methods of any one of claims 39 to 41.

43.   A pharmaceutical composition comprising the compound of claim 42.

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44.   A method for the preparation of the pharmaceutical composition of claim 43 comprising formulating the compound of claim 42 in a pharmaceutically acceptable carrier or diluent.

10   45.   Use of a compound of claim 42 for the preparation of a medicament for the treatment or prevention of pancreatic cancer.

46.   Use of a compound of claim 42 for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer.

15

47.   The use of claim 45 or 46 wherein said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

20   48.   Antibodies against the proteins listed in tables 5 and/or 6, or antigen-binding fragments thereof, for the use in an in vitro method for the diagnosis of pancreatic cancer.

49.   A kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, of claim 48.

25

50.   A kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker of claims 26 to 28.

51.   A kit for screening of compounds that activate or inhibit any of the polypeptides listed in table 5 and/or 6, or stimulate or inhibit the expression of any of said polypeptides.

5

52.   The kit of claim 51, wherein said polypeptides are the polypeptides listed in table 6.

53.   The proteins, compounds, kits, methods and uses substantially as herein before described, especially with reference to the foregoing examples.

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SEQUENCE LISTING

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Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Ile His Cys Lys Leu
            100                 105                 110
Leu Asp Ile Ala Cys Trp Ile His His Lys Tyr Asn Ser Asp Lys Ser
        115                 120                 125
Ser Thr Tyr Val Lys Asn Gly Thr Ser Phe Asp Ile His Tyr Gly Ser
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Gly Ser Leu Ser Gly Tyr Leu Ser Gln Asp Thr Val Ser Val Pro Cys
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Gln Ser Ala Ser Ser Ala Leu Gly Gly Val Lys Val Glu Arg
        165                 170                 175
Gln Val Phe Gly Glu Ala Thr Lys Gln Pro Gly Ile Thr Phe Ile Ala
            180                 185                 190
Ala Lys Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro Arg Ile Ser Val
        195                 200                 205
Asn Asn Val Leu Pro Val Phe Asp Asn Leu Met Gln Gln Lys Leu Val
            210                 215                 220
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Pro Gly Gly Glu Met Leu Gly Gly Thr Asp Ser Lys Tyr Tyr Lys
            245                 250                 255
Gly Ser Leu Ser Tyr Leu Asn Val Thr Arg Lys Ala Tyr Trp Gln Val
            260                 265                 270
His Leu Asp Gln Val Glu Val Ala Ser Gly Leu Thr Leu Cys Lys Glu
    275                 280                 285
Gly Cys Glu Ala Ile Val Asp Thr Gly Thr Ser Leu Met Val Gly Pro
    290                 295                 300
Val Asp Val Arg Glu Leu Gln Lys Ala Ile Gly Ala Val Pro Leu
    305         310                 315                 320
Ile Gln Gly Glu Tyr Met Ile Pro Cys Glu Lys Val Ser Thr Leu Pro
            325                 330                 335
Ala Ile Leu Lys Leu Gly Leu Gly Lys Gly Tyr Lys Leu Ser Pro Glu
            340                 345                 350
Asp Tyr Thr Leu Lys Val Ser Gln Ala Gly Lys Thr Leu Cys Leu Ser
            355                 360                 365
Gly Phe Met Gly Met Asp Ile Pro Pro Ser Gly Pro Leu Trp Ile
            370                 375                 380
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    35                  40                  45
Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu Ala Ile
50                  55                  60
Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro Asp Glu
65                  70                  75                  80
Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser Pro Asn
            85                  90                  95
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            100                 105                 110
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Gly Val Ala Met Gly Met Tyr Asn Gln Asp Lys Ser Ile Glu Asp Phe
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Ala His Ser Ser Phe Gln Met Ala Leu Ser Lys Gly Trp Pro Leu Tyr
195   200   205

Leu Ser Thr Lys Asn Thr Ile Leu Lys Tyr Asp Gly Arg Phe Lys
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Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln Phe Glu
225   230   235   240

Ala Gln Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met Val Ala
245   250   255

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275   280   285

Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr Val Glu
290   295   300

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Lys Gly Gln Glu Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe Ala Trp
325   330   335

5 Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys Glu Leu
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Ala Gly Phe Met Thr Lys Asp Leu Ala Ala Cys Ile Lys Gly Leu Pro
10   370   375   380

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Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
65                  70                  75                  80
Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
                85                  90                  95
Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
            100                 105                 110
His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
            115                 120                 125
Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
        130                 135                 140
Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
145                 150                 155                 160
Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe
                165                 170                 175
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Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala
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Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser
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Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro
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Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His
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Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys
            355                 360                 365
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Glu Thr Pro Leu Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp
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Gln Thr Asp Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn
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Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Ser Thr Ala
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Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln
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Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr
    450   455   460

Tyr Gly Gln Phe Tyr Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr
    465   470   475   480

Arg His Gly Arg Gly Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala
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Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln
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Leu Asp Glu Glu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln
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Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met
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    545   550   555   560

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    565   570   575

Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp
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Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr
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Gly Ala Ser Glu Ala Lys Thr Gly Ala Gln Glu Leu Leu Arg Val
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Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly
10 625   630   635   640

Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg
    645   650   655

Leu Lys Asp Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys
    660   665   670

Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Val Pro Gly Glu Leu
15 675   680   685

Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp
    690   695   700

Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Lys
20 705   710   715   720

Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala
    725   730   735

Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu
    740   745   750

Pro Pro Ser Phe Val Gly Trp Phe Gly Trp Asp Asp Asp Tyr Trp
      755   760   765

Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala
      770   775   780
5

<210> 4
<211> 764
<212> PRT
<213> Homo sapiens
10
<220>
<221> Complement factor B precursor
<222> (1)..(764)
<223> Accession No. as of 06 Dec 2002: P00751
15 <400> 4

Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1   5   10   15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
20   25   30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
      35   40   45

Phe Arg Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
50   55   60

Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65   70   75   80

Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
      85   90   95

5 Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
        100   105   110

Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
      115   120   125

Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
10   130   135   140

Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
      145   150   155   160

Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
        165   170   175

15 Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
        180   185   190

Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
      195   200   205

Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
20   210   215   220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
      225   230   235   240

Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
        245   250   255

```
     Gln Lys Arg Lys Ile Val Asp Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
                 260                 265                 270

     Leu Val Leu Asp Gly Ser Asp Ser Ile Gly Ala Ser Asn Phe Thr Gly
                 275                 280                 285

 5   Ala Lys Lys Cys Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
                 290                 295                 300

     Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
             305                 310                 315             320

     Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
                 325                 330                 335

10   Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
                 340                 345                 350

     Thr Asn Thr Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
                 355                 360                 365

15   Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
                 370                 375                 380

     Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
             385                 390                 395             400

     Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
                 405                 410                 415

20   Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
                 420                 425                 430

     Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
                 435                 440                 445
```

```
     Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
                 450                 455                 460

     Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
             465                 470                 475             480

 5   Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                 485                 490                 495

     Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
                 500                 505                 510

     Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
                 515                 520                 525

10   Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
                 530                 535                 540

     Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
             545                 550                 555             560

15   Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                 565                 570                 575

     Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
                 580                 585                 590

     Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
                 595                 600                 605

20   Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
                 610                 615                 620

     Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
             625                 630                 635             640
```

Thr Arg Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
             645   650   655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
             660   665   670

5   Ser Glu Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Val Ser Pro
             675   680   685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
             690   695   700

Val His Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
10   705   710   715   720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
             725   730   735

His Ala Arg Asp His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
             740   745   750

15 Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu
             755   760

<210> 5
20 <211> 911
   <212> PRT
   <213> Homo sapiens
   <220>
   <221> Alpha-actinin 4

<222> (1)..(911)
<223> Accession No. O43707
<400> 5

5   Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser
   1   5   10   15

Ser Ala Gly Asn Gly Ala Gly Gly Gly Gly Ser Met Gly Asp Tyr Met
             20   25   30

Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp
10   35   40   45

Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu
             50   55   60

Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Glu Asp Phe Arg Asp
65   70   75   80

15 Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu
             85   90   95

Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val
             100   105   110

Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser
20   115   120   125

Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly
             130   135   140

Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val
             145   150   155   160

```
   Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys
                   165              170              175

   Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp
                   180              185              190

 5 Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu
                   195              200              205

   Leu Ile Glu Tyr Asp Lys Leu Arg Arg Lys Asp Asp Pro Val Thr Asn Leu
               210              215              220

   Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met
10             225              230              235              240

   Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala
               245              250              255

   Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln
               260              265              270

15 Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn
               275              280              285

   Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp
               290              295              300

   Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp Arg Val
20             305              310              315              320

   Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp Phe Arg
               325              330              335

   Asp Tyr Arg Arg His Lys Pro Pro Val Gln Glu Lys Cys Gln
               340              345              350
```

```
   Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn
                   355              360              365

   Arg Pro Ala Phe Met Pro Ser Gly Lys Met Val Ser Asp Ile Asn
               370              375              380

 5 Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu Glu Trp
               385              390              395              400

   Leu Leu Asn Glu Ile Arg Arg Glu Leu Asp Arg His Leu Ala Glu
               405              410              415

   Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys
10             420              425              430

   Glu Ala Met Lys His Arg Asp Tyr Glu Thr Ala Thr Leu Ser Asp
               435              440              445

   Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp Leu Ala
               450              455              460

15 Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu
               465              470              475              480

   Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg Cys Gln
               485              490              495

   Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His Ser Arg
20             500              505              510

   Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile Asp Gln
               515              520              525

   Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met
               530              535              540
```

Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val His Thr Ile
    545   550   555   560

Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr
      565   570   575

5 Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys
      580   585   590

Gln Ala Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser
      595   600   605

Asn Pro Tyr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu
10   610   615   620

Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu
      625   630   635   640

Gln Ser Lys Gln Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser
      645   650   655

15 Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile
      660   665   670

Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser
      675   680   685

His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu
20   690   695   700

Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe
      705   710   715   720

Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp
      725   730   735

Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn
      740   745   750

Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Gln
      755   760   765

5 Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly Gly Ala
      770   775   780

Leu Gly Pro Glu Phe Lys Ala Cys Ile Ser Leu Gly Tyr Asp
      785   790   795   800

Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe Asn Arg Ile Met Ser
10   805   810   815

Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe Ile
      820   825   830

Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln Val
      835   840   845

15 Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr Ala
      850   855   860

Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile
      865   870   875   880

Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val Pro Gly Ala Leu
20   885   890   895

Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
      900   905   910

<210> 6
<211> 683
<212> PRT
<213> Homo sapiens

<220>
<221> Transforming growth factor-beta induced protein IG-H3 precursor
<222> (1)..(683)
<223> Accession No. as of 06 Dec 2002: Q15582

<400> 6

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Met Ala Leu Phe Val Arg Leu Leu Ala Leu Ala Leu Ala Leu Ala Leu
1               5                   10                  15

Gly Pro Ala Ala Thr Leu Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu
            20                  25                  30

Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val
15          35                  40                  45

Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn
            50                  55                  60

Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile
65          70                  75                  80

Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly
            85                  90                  95

Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val
            100                 105                 110
```

```
Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
                115                 120                 125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Ile Phe Ala Pro Ser
            130                 135                 140

Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val
5   145                 150                 155                 160

Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val
                165                 170                 175

Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr
10                  180                 185                 190

Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly
                195                 200                 205

Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala
                210                 215                 220

Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr
15              225                 230                 235         240

Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu
                245                 250                 255

Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn
20              260                 265                 270

Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile
                275                 280                 285

Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg
                290                 295                 300
```

```
Asp Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala
305              310              315              320

Ile Val Ala Gly Leu Ser Glu Val Glu Thr Leu Glu Gly Thr Leu Glu
            325              330              335

5  Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile
            340              345              350

Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp
            355              360              365

Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala
            370              375              380

Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu
            385              390              395              400

Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu
            405              410              415

15 Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg
            420              425              430

Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr
            435              440              445

Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg
            450              455              460

20 Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala
            465              470              475              480

Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg
            485              490              495
```

```
Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp
500              505              510

Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr
            515              520              525

5  Glu Thr Leu Asn Arg Glu Gly Val Gly Val Tyr Thr Val Phe Ala Pro Thr Asn
            530              535              540

Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Gly
            545              550              555              560

Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu
            565              570              575

10 Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu
            580              585              590

Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val
            595              600              605

15 Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val
            610              615              620

Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln
            625              630              635              640

Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln
            645              650              655

20 Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro
            660              665              670

Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His
            675              680
```

<210> 7
<211> 892
<212> PRT
<213> Homo sapiens

<220>
<221> Alpha-actinin 1
<222> (1)..(892)
<223> Accession No. P12814

<400> 7

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Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu
1               5                   10                  15
Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln
15              20                  25                  30
Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala
            35                  40                  45
Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys
    50                  55                  60
Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro
65                  70                  75                  80
Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala
                85                  90                  95
```

```
Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala
                100                 105                 110
Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp
                115                 120                 125
Thr Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr
5               130                 135                 140
Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro
            145                 150                 155                 160
Tyr Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly
            165                 170                 175
Leu Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp
10          180                 185                 190
Tyr Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala
            195                 200                 205
Phe Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala
15          210                 215                 220
Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr
            225                 230                 235                 240
Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu
            245                 250                 255
Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn
            260                 265                 270
Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu
            275                 280                 285
```

Trp Ile Arg Arg Thr Ile Pro Trp Glu Asn Arg Val Pro Glu Asn

 290   295   300

Thr Met His Ala Met Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg

 305   310   315   320

Arg Leu His Lys Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile

 5   325   330   335

Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala

         340   345   350

Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp Ile Asn Asn Ala Trp

 10   355   360   365

Gly Cys Leu Glu Gln Val Glu Lys Gly Tyr Glu Trp Leu Leu Asn

         370   375   380

Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Ala Glu Lys Phe Arg

 385   390   395   400

Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met

 15   405   410   415

Leu Arg Gln Lys Asp Tyr Glu Thr Ala Thr Leu Ser Glu Ile Lys Ala

         420   425   430

Leu Leu Lys His Glu Ala Phe Glu Ser Asp Leu Leu Asn Glu Leu

 20   435   440   445

Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu Asn Glu Leu

 450   455   460

Asp Tyr Tyr Asp Ser Pro Ser Val Asn Ala Arg Cys Gln Lys Ile Cys

 465   470   475   480

Asp Gln Trp Asp Asn Leu Gly Ala Leu Thr Gln Lys Arg Arg Glu Ala

                 485   490   495

Leu Glu Arg Thr Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu

                 500   505   510

Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala

 5   515   520   525

Met Glu Asp Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile

                 530   535   540

Gln Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp

 10 545   550   555   560

Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile Ile His Asn Glu Val Ser

                 565   570   575

Lys Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr

                 580   585   590

Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg

 15   595   600   605

Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg

                 610   615   620

Gln Gln His Asn Glu Ser Val Arg Lys Gln Phe Gly Ala Gln Ala Asn

 20 625   630   635   640

Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile

                 645   650   655

Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg

                 660   665   670

```
Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu
                675                 680                 685

      Glu Gly Asp His Gln Leu Ile Gln Ala Leu Ile Phe Asp Asn Lys
                690                 695                 700

 5    His Thr Asn Tyr Thr Met Glu His Ile Arg Arg Val Gly Trp Glu Gln Leu
                705                 710                 715                 720

      Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu
                            725                 730                 735

      Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg
10                          740                 745                 750

      Ala Ser Phe Asn His Phe Asp Arg Asp His Ser Gly Thr Leu Gly Pro
                            755                 760                 765

      Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp Ile Gly Asn
                            770                 775                 780

15    Asp Pro Gln Gly Glu Ala Glu Phe Ala Arg Ile Met Ser Ile Val Asp
                            785                 790                 795                 800

      Pro Asn Arg Leu Gly Val Val Thr Phe Gln Ala Phe Ile Asp Phe Met
                            805                 810                 815

      Ser Arg Glu Thr Ala Asp Thr Asp Thr Ala Asp Gln Val Met Ala Ser
20                          820                 825                 830

      Phe Lys Ile Leu Ala Gly Asp Lys Asn Tyr Ile Thr Met Asp Glu Leu
                            835                 840                 845

      Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met
                            850                 855                 860
```

```
      Ala Pro Tyr Thr Gly Pro Asp Ser Val Pro Gly Ala Leu Asp Tyr Met
                865                 870                 875                 880

      Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
                            885                 890

 5

      <210>   8
      <211>   448
      <212>   PRT
10    <213>   Homo sapiens

      <220>
      <221>   Tubulin alpha-4 chain
      <222>   (1)..(448)
      <223>   Accession No. P05215

15    <400>   8

      Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln Met
      1                 5                   10                  15

      Gly Asn Ala Cys Trp Glu Leu Tyr Cys Leu Glu His Gly Ile Gln Pro
                  20                  25                  30

20    Asp Gly Gln Met Pro Ser Asp Lys Thr Ile Gly Gly Gly Asp Asp Ser
                  35                  40                  45

      Phe Thr Phe Phe Cys Glu Thr Gly Ala Gly Lys His Val Pro Arg
              50                  55                  60
```

```
Ala Val Phe Val Asp Leu Glu Pro Thr Val Ile Asp Glu Ile Arg Asn
            65              70              75              80

Gly Pro Tyr Arg Gln Leu Phe His Pro Glu Gln Leu Ile Thr Gly Lys
                    85              90              95

Glu Asp Ala Ala Asn Asn Tyr Ala Arg Gly His Tyr Thr Ile Gly Lys
5                       100             105             110

Glu Ile Ile Asp Pro Val Leu Asp Arg Ile Arg Lys Leu Ser Asp Gln
                    115             120             125

Cys Thr Gly Leu Gln Gly Phe Leu Val Phe His Ser Phe Gly Gly Gly
10                      130             135             140

Thr Gly Ser Gly Phe Ser Leu Leu Met Glu Arg Leu Ser Val Asp
                    145             150             155             160

Tyr Gly Lys Lys Ser Lys Leu Glu Phe Ser Ile Tyr Pro Ala Pro Gln
                    165             170             175

Val Ser Thr Ala Val Val Glu Pro Tyr Asn Ser Ile Leu Thr Thr His
15                      180             185             190

Thr Thr Leu Glu His Ser Asp Cys Ala Phe Met Val Asp Asn Glu Ala
                    195             200             205

Ile Tyr Asp Ile Cys Arg Arg Asn Leu Asp Ile Glu Arg Pro Thr Tyr
                    210             215             220

Thr Asn Leu Asn Arg Leu Ile Ser Gln Ile Val Ser Ser Ile Thr Ala
20                      225             230             235             240

Ser Leu Arg Phe Asp Gly Ala Leu Asn Val Asp Leu Thr Glu Phe Gln
                    245             250             255
```

```
Thr Asn Leu Val Pro Tyr Pro Arg Ile His Phe Pro Leu Ala Thr Tyr
                    260             265             270

Ala Pro Val Ile Ser Ala Glu Lys Ala Tyr His Glu Gln Leu Ser Val
                    275             280             285

Ala Glu Ile Thr Asn Ala Cys Phe Glu Pro Ala Asn Gln Met Val Lys
5                       290             295             300

Cys Asp Pro Arg His Gly Lys Tyr Met Ala Cys Cys Leu Leu Tyr Arg
                    305             310             315             320

Gly Asp Val Val Pro Lys Asp Val Asn Ala Ala Ile Ala Ala Ile Lys
10                      325             330             335

Thr Lys Arg Ser Ile Gln Phe Val Asp Trp Cys Pro Thr Gly Phe Lys
                    340             345             350

Val Gly Ile Asn Tyr Gln Pro Pro Thr Val Val Pro Gly Gly Asp Leu
                    355             360             365

Ala Lys Val Gln Arg Ala Val Cys Met Leu Ser Asn Thr Thr Ala Ile
15                      370             375             380

Ala Glu Ala Trp Ala Arg Leu Asp His Lys Phe Asp Leu Met Tyr Ala
                    385             390             395             400

Lys Arg Ala Phe His His Trp Tyr Val Gly Glu Gly Met Glu Glu Gly
                    405             410             415

Glu Phe Ser Glu Ala Arg Glu Asp Met Ala Ala Leu Glu Lys Asp Tyr
                    420             425             430

Glu Glu Val Gly Ile Asp Ser Tyr Glu Asp Glu Asp Glu Gly Glu Glu
                    435             440             445
```

```
<210>   9
<211>   2647
<212>   PRT
<213>   Homo sapiens

<220>
<221>   Filamin A
<222>   (1)..(2647)
<223>   Accession No. P21333

<400>   9

Met Ser Ser His Ser Arg Ala Gly Gln Ser Ala Ala Gly Ala Ala
1               5               10              15

Pro Gly Gly Val Asp Thr Arg Asp Ala Glu Met Pro Ala Thr Glu
                20              25              30

Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys Ile Gln Gln Asn Thr
                35              40              45

Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Ser Lys Arg Ile
        50              55              60

Ala Asn Leu Gln Thr Asp Leu Ser Asp Gly Leu Arg Leu Ile Ala Leu
        65              70              75              80

Leu Glu Val Leu Ser Gln Lys Lys Met His Arg Lys His Asn Gln Arg
                85              90              95
```

```
Pro Thr Phe Arg Gln Met Gln Leu Glu Asn Val Ser Val Ala Leu Glu
                100             105             110

Phe Leu Asp Arg Glu Ser Ile Lys Leu Val Ser Ile Asp Ser Lys Ala
            115             120             125

Ile Val Asp Gly Asn Leu Lys Leu Ile Leu Gly Leu Ile Trp Thr Leu
5           130             135             140

Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp Asp Glu Glu Asp
            145             150             155             160

Glu Glu Ala Lys Lys Gln Thr Pro Lys Gln Arg Leu Leu Gly Trp Ile
            165             170             175

Gln Asn Lys Leu Pro Gln Leu Pro Ile Thr Asn Phe Ser Arg Asp Trp
10          180             185             190

Gln Ser Gly Arg Ala Leu Gly Ala Leu Val Asp Ser Cys Ala Pro Gly
            195             200             205

Leu Cys Pro Asp Trp Asp Ser Trp Asp Ala Ser Lys Pro Val Thr Asn
15          210             215             220

Ala Arg Glu Ala Met Gln Ala Asp Asp Trp Leu Gly Ile Pro Gln
            225             230             235             240

Val Ile Thr Pro Glu Ile Val Asp Pro Asn Val Asp Glu His Ser
            245             250             255

Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys Pro Gly
20          260             265             270

Ala Pro Leu Arg Pro Lys Leu Asn Pro Lys Ala Arg Ala Tyr Gly
            275             280             285
```

Pro Gly Ile Glu Pro Thr Gly Asn Met Val Lys Lys Arg Ala Glu Phe
    290   295   300

Thr Val Glu Thr Arg Ser Ala Gly Gln Gly Glu Val Leu Val Tyr Val
    305   310   315   320

5   Glu Asp Pro Ala Gly His Gln Glu Glu Ala Lys Val Thr Ala Asn Asn
    325   330   335

Asp Lys Asn Arg Thr Phe Ser Val Trp Tyr Val Pro Glu Val Thr Gly
    340   345   350

10 Thr His Lys Val Thr Val Leu Phe Ala Gly Gln His Ile Ala Lys Ser
    355   360   365

Pro Phe Glu Val Tyr Val Asp Ser Lys Ser Gln Gly Asp Ala Ser Lys Val
    370   375   380

Thr Ala Gln Gly Pro Gly Leu Glu Pro Ser Gly Asn Ile Ala Asn Lys
    385   390   395   400

15 Thr Thr Tyr Phe Glu Ile Phe Thr Ala Gly Ala Gly Thr Gly Glu Val
    405   410   415

Glu Val Ile Gln Asp Pro Met Gly Gln Lys Gly Thr Val Glu Pro
    420   425   430

Gln Leu Glu Ala Arg Gly Asp Ser Thr Tyr Arg Cys Ser Tyr Gln Pro
    435   440   445

20 Thr Met Glu Gly Val His Thr Val His Val Thr Phe Ala Gly Val Pro
    450   455   460

Ile Pro Arg Ser Pro Tyr Thr Val Thr Val Gly Gln Ala Cys Asn Pro
    465   470   475   480

Ser Ala Cys Arg Ala Val Gly Arg Gly Leu Gln Pro Lys Gly Val Arg
    485   490   495

Val Lys Glu Thr Ala Asp Lys Val Tyr Thr Lys Gly Ala Gly Ser
    500   505   510

5   Gly Glu Leu Lys Val Thr Val Lys Gly Pro Lys Gly Glu Glu Arg Val
    515   520   525

Lys Gln Lys Asp Leu Gly Asp Gly Val Tyr Gly Phe Glu Tyr Tyr Pro
    530   535   540

10 Met Val Pro Gly Thr Tyr Ile Val Thr Ile Thr Trp Gly Gly Gln Asn
    545   550   555   560

Ile Gly Arg Ser Pro Phe Glu Val Lys Val Gly Thr Glu Cys Gly Asn
    565   570   575

Gln Lys Val Arg Ala Trp Gly Pro Gly Leu Glu Gly Gly Val Val Gly
    580   585   590

15 Lys Ser Ala Asp Phe Val Glu Ala Ile Gly Asp Asp Val Gly Thr
    595   600   605

Leu Gly Phe Ser Val Glu Gly Pro Ser Gln Ala Lys Ile Glu Cys Asp
    610   615   620

Asp Lys Gly Asp Gly Ser Cys Asp Val Arg Tyr Trp Pro Gln Glu Ala
    625   630   635   640

20 Gly Glu Tyr Ala Val His Val Leu Cys Asn Ser Glu Asp Ile Arg Leu
    645   650   655

Ser Pro Phe Met Ala Asp Ile Arg Asp Ala Pro Gln Asp Phe His Pro
    660   665   670

```
Asp Arg Lys Ala Arg Gly Pro Gly Leu Glu Lys Thr Gly Val Ala
        675             680              685

Val Asn Lys Pro Ala Glu Phe Thr Val Asp Lys His Gly Gly Lys
        690             695             700

5   Ala Pro Leu Arg Val Gln Val Gln Asp Asn Glu Gly Cys Pro Val Glu
        705             710             715             720

Ala Leu Val Lys Asp Asn Gly Asn Gly Thr Tyr Ser Cys Ser Tyr Val
        725             730             735

Pro Arg Lys Pro Val His Thr Ala Met Val Ser Trp Gly Gly Val
10      740             745             750

Ser Ile Pro Asn Ser Pro Phe Arg Val Asn Val Gly Ala Gly Ser His
        755             760             765

Pro Asn Lys Val Lys Val Tyr Gly Pro Gly Val Ala Lys Thr Gly Leu
        770             775             780

15  Lys Ala His Glu Pro Thr Tyr Phe Thr Val Asp Cys Ala Glu Ala Gly
        785             790             795             800

Gln Gly Asp Val Ser Ile Gly Ile Lys Cys Ala Pro Gly Val Val Gly
                    805             810             815

Pro Ala Glu Ala Asp Ile Asp Phe Asp Ile Arg Asn Asp Asn Asp
20      820             825             830

Thr Phe Thr Val Lys Tyr Thr Pro Arg Gly Ala Gly Ser Tyr Thr Ile
        835             840             845

Met Val Leu Phe Ala Asp Gln Ala Thr Pro Thr Ser Pro Ile Arg Val
        850             855             860
```

```
Lys Val Glu Pro Ser His Asp Ala Ser Lys Val Lys Ala Glu Gly Pro
        865             870             875             880

Gly Leu Ser Arg Thr Gly Val Glu Leu Gly Lys Pro Thr His Phe Thr
                    885             890             895

5   Val Asn Ala Lys Ala Ala Gly Lys Gly Lys Leu Asp Val Gln Phe Ser
                    900             905             910

Gly Leu Thr Lys Gly Asp Ala Val Arg Asp Val Asp Ile Ile Asp His
                    915             920             925

His Asp Asn Thr Tyr Thr Val Lys Tyr Thr Pro Val Gln Gln Gly Pro
10      930             935             940

Val Gly Val Asn Val Thr Tyr Gly Gly Asp Pro Ile Pro Lys Ser Pro
        945             950             955             960

Phe Ser Val Ala Val Ser Pro Ser Leu Asp Ser Lys Ile Lys Val
        965             970             975

15  Ser Gly Leu Gly Glu Lys Val Asp Val Gly Lys Asp Gln Glu Phe Thr
        980             985             990

Val Lys Ser Lys Gly Ala Gly Gly Gln Gly Lys Val Ala   Ser Lys Ile
                    995             1000             1005

Val Gly Pro Ser Gly Ala Ala Val Pro Cys Lys Val Glu Pro Gly
20      1010             1015             1020

Leu Gly Ala Asp Asn Ser Val Val Arg Phe Leu Pro Arg Glu Glu
                    1025             1030             1035

Gly Pro Tyr Glu Val Glu Val Thr Tyr Asp Gly Val Pro Val Pro
                    1040             1045             1050
```

Gly Ser Pro Phe Pro Leu Glu Ala Val Ala Pro Thr Lys Pro Ser
1055   1060   1065

Lys Val Lys Ala Phe Gly Pro Gly Leu Gln Gly Gly Ser Ala Gly
1070   1075   1080

Ser Pro Ala Arg Phe Thr Ile Asp Thr Lys Gly Ala Gly Thr Gly
1085   1090   1095

Gly Leu Gly Leu Thr Val Glu Gly Pro Cys Glu Ala Gln Leu Glu
1100   1105   1110

Cys Leu Asp Asn Gly Asp Gly Thr Cys Ser Val Ser Tyr Val Pro
1115   1120   1125

Thr Glu Pro Gly Asp Tyr Asn Ile Asn Ile Leu Phe Ala Asp Thr
1130   1135   1140

His Ile Pro Gly Ser Pro Phe Lys Ala His Val Val Pro Cys Phe
1145   1150   1155

Asp Ala Ser Lys Val Lys Cys Ser Gly Pro Gly Leu Glu Arg Ala
1160   1165   1170

Thr Ala Gly Glu Val Gly Gln Phe Gln Val Asp Cys Ser Ser Ala
1175   1180   1185

Gly Ser Ala Glu Leu Thr Ile Glu Ile Cys Ser Glu Ala Gly Leu
1190   1195   1200

Pro Ala Glu Val Tyr Ile Gln Asp His Gly Asp Gly Thr His Thr
1205   1210   1215

Ile Thr Tyr Ile Pro Leu Cys Pro Gly Ala Tyr Thr Val Thr Ile
1220   1225   1230

Lys Tyr Gly Gly Gln Pro Val Pro Asn Phe Pro Ser Lys Leu Gln
1235   1240   1245

Val Glu Pro Ala Val Asp Thr Ser Gly Val Gln Cys Tyr Gly Pro
1250   1255   1260

Gly Ile Glu Gly Gln Gly Val Phe Arg Glu Ala Thr Thr Glu Phe
1265   1270   1275

Ser Val Asp Ala Arg Ala Leu Thr Gln Thr Gly Gly Pro His Val
1280   1285   1290

Lys Ala Arg Val Ala Asn Pro Ser Gly Asn Leu Thr Glu Thr Tyr
1295   1300   1305

Val Gln Asp Arg Gly Asp Gly Met Tyr Lys Val Glu Tyr Thr Pro
1310   1315   1320

Tyr Glu Gly Leu His Ser Val Asp Val Thr Tyr Asp Gly Ser
1325   1330   1335

Pro Val Pro Ser Ser Pro Phe Gln Val Pro Val Thr Glu Gly Cys
1340   1345   1350

Asp Pro Ser Arg Val Arg Val His Gly Pro Gly Ile Gln Ser Gly
1355   1360   1365

Thr Thr Asn Lys Pro Asn Lys Phe Thr Val Glu Thr Arg Gly Ala
1370   1375   1380

Gly Thr Gly Gly Leu Gly Leu Ala Val Glu Gly Pro Ser Glu Ala
1385   1390   1395

Lys Met Ser Cys Met Asp Asn Lys Asp Gly Ser Cys Ser Val Glu
1400   1405   1410

```
   Thr His  Ile Gln Asp Asn His  Asp Gly Thr Tyr Thr  Val Ala Tyr
                      1595            1600              1605
 5 Val Pro  Asp Val Thr Gly Arg  Tyr Thr Ile Leu Ile  Lys Tyr Gly
                      1610            1615              1620
   Gly Asp  Glu Ile Pro Phe Ser  Pro Tyr Arg Val Arg  Ala Val Pro
                      1625            1630              1635
   Thr Gly  Asp Ala Ser Lys Cys  Thr Val Thr Val Ser  Ile Gly Gly
10                    1640            1645              1650
   His Gly  Leu Gly Ala Gly Ile  Gly Pro Thr Ile Gln  Ile Gly Glu
                      1655            1660              1665
   Glu Thr  Val Ile Thr Val Asp  Thr Lys Ala Ala Gly  Lys Gly Lys
                      1670            1675              1680
15 Val Thr  Cys Thr Val Cys Thr  Pro Asp Gly Ser Glu  Val Asp Val
                      1685            1690              1695
   Asp Val  Val Glu Asn Glu Asp  Gly Thr Phe Asp Ile  Phe Tyr Thr
                      1700            1705              1710
   Ala Pro  Gln Pro Gly Lys Tyr  Val Ile Cys Val Arg  Phe Gly Gly
20                    1715            1720              1725
   Glu His  Val Pro Asn Ser Pro  Phe Gln Val Thr Ala  Leu Ala Gly
                      1730            1735              1740
   Asp Gln  Pro Ser Val Gln Pro  Pro Leu Arg Ser Gln  Gln Leu Ala
                      1745            1750              1755
```

```
   Tyr Ile  Pro Tyr Glu Ala Gly  Thr Tyr Ser Leu Asn  Val Thr Tyr
                      1415            1420              1425
   Gly Gly  His Gln Val Pro Gly  Ser Pro Phe Lys Val  Pro Val His
                      1430            1435              1440
 5 Asp Val  Thr Asp Ala Ser Lys  Val Lys Cys Ser Gly  Pro Gly Leu
                      1445            1450              1455
   Ser Pro  Gly Met Val Arg Ala  Asn Leu Pro Gln Ser  Phe Gln Val
                      1460            1465              1470
   Asp Thr  Ser Lys Ala Gly Val  Ala Pro Leu Gln Val  Lys Val Gln
10                    1475            1480              1485
   Gly Pro  Lys Gly Leu Val Glu  Pro Val Asp Val Val  Asp Asn Ala
                      1490            1495              1500
   Asp Gly  Thr Gln Thr Val Asn  Tyr Val Pro Ser Arg  Glu Gly Pro
                      1505            1510              1515
15 Tyr Ser  Ile Ser Val Leu Tyr  Gly Asp Glu Glu Val  Pro Arg Ser
                      1520            1525              1530
   Pro Phe  Lys Val Lys Val Leu  Pro Thr His Asp Ala  Ser Lys Val
                      1535            1540              1545
   Lys Ala  Ser Gly Pro Gly Leu  Asn Thr Thr Gly Val  Pro Ala Ser
20                    1550            1555              1560
   Leu Pro  Val Glu Phe Thr Ile  Asp Ala Lys Asp Ala  Gly Glu Gly
                      1565            1570              1575
   Leu Leu  Ala Val Gln Ile Thr  Asp Pro Glu Gly Lys  Pro Lys Lys
                      1580            1585              1590
```

Pro Gln Tyr Thr Tyr Ala Gln Gly Gly Gln Thr Trp Ala Pro
    1760   1765   1770

Glu Arg Pro Leu Val Gly Val Asn Gly Leu Asp Val Thr Ser Leu
    1775   1780   1785

Arg Pro Asp Leu Val Ile Pro Phe Thr Ile Lys Lys Gly Glu
5   1790   1795   1800

Ile Thr Gly Glu Val Arg Met Pro Ser Gly Lys Val Ala Gln Pro
    1805   1810   1815

Thr Ile Thr Asp Asn Lys Asp Gly Thr Val Thr Val Arg Tyr Ala
10   1820   1825   1830

Pro Ser Glu Ala Gly Leu His Glu Met Asp Ile Arg Tyr Asp Asn
    1835   1840   1845

Met His Ile Pro Gly Ser Pro Leu Gln Phe Tyr Val Asp Tyr Val
    1850   1855   1860

Asn Cys Gly His Val Thr Ala Tyr Gly Pro Gly Leu Thr His Gly
15   1865   1870   1875

Val Val Asn Lys Pro Ala Thr Phe Thr Val Asn Thr Lys Asp Ala
    1880   1885   1890

Gly Glu Gly Gly Leu Ser Leu Ala Ile Glu Gly Pro Ser Lys Ala
    1895   1900   1905

Glu Ile Ser Cys Thr Asp Asn Gln Asp Gly Thr Cys Ser Val Ser
20   1910   1915   1920

Tyr Leu Pro Val Leu Pro Gly Asp Tyr Ser Ile Leu Val Lys Tyr
    1925   1930   1935

Asn Glu Gln His Val Pro Gly Ser Pro Phe Thr Ala Arg Val Thr
    1940   1945   1950

Gly Asp Asp Ser Met Arg Met Ser His Leu Lys Val Gly Ser Ala
    1955   1960   1965

Ala Asp Ile Pro Ile Asn Ile Ser Glu Thr Asp Leu Ser Leu Leu
5   1970   1975   1980

Thr Ala Thr Val Val Pro Pro Ser Gly Arg Glu Glu Pro Cys Leu
    1985   1990   1995

Leu Lys Arg Leu Arg Asn Gly His Val Gly Ile Ser Phe Val Pro
10   2000   2005   2010

Lys Glu Thr Gly Glu His Leu Val His Val Lys Lys Asn Gly Gln
    2015   2020   2025

His Val Ala Ser Ser Pro Ile Pro Val Val Ile Ser Gln Ser Glu
    2030   2035   2040

Ile Gly Asp Ala Ser Arg Val Arg Val Ser Gly Gln Gly Leu His
15   2045   2050   2055

Glu Gly His Thr Phe Glu Pro Ala Glu Phe Ile Ile Asp Thr Arg
    2060   2065   2070

Asp Ala Gly Tyr Gly Gly Leu Ser Leu Ser Ile Glu Gly Pro Ser
20   2075   2080   2085

Lys Val Asp Ile Asn Thr Glu Asp Leu Glu Asp Gly Thr Cys Arg
    2090   2095   2100

Val Thr Tyr Cys Pro Thr Glu Pro Gly Asn Tyr Ile Ile Asn Ile
    2105   2110   2115

```
Lys Phe  Ala Asp Gln His Val  Pro Gly Ser Pro Phe  Ser Val Lys
                        2120                2125              2130
Val Thr  Gly Glu Gly Arg Val  Lys Glu Ser Ile Thr  Arg Arg Arg
                        2135                2140              2145
Arg Ala  Pro Ser Val Ala Asn  Val Gly Ser His Cys  Asp Leu Ser
5                       2150                2155              2160
Leu Lys  Ile Pro Glu Ile Ser  Ile Gln Asp Met Thr  Ala Gln Val
                        2165                2170              2175
Thr Ser  Pro Ser Gly Lys Thr  His Glu Ala Glu Ile  Val Glu Gly
10                      2180                2185              2190
Glu Asn  His Thr Tyr Cys Ile  Arg Phe Val Pro Ala  Glu Met Gly
                        2195                2200              2205
Thr His  Thr Val Ser Val Lys  Tyr Lys Gly Gln His  Val Pro Gly
                        2210                2215              2220
Ser Pro  Phe Gln Phe Thr Val  Gly Pro Leu Gly Glu  Gly Gly Ala
15                      2225                2230              2235
His Lys  Val Arg Ala Gly Gly  Pro Gly Leu Glu Arg  Ala Glu Ala
                        2240                2245              2250
Gly Val  Pro Ala Glu Phe Ser  Ile Trp Thr Arg Glu  Ala Gly Ala
                        2255                2260              2265
Gly Gly  Leu Ala Ile Ala Val  Glu Gly Pro Ser Lys  Ala Glu Ile
20                      2270                2275              2280
Ser Phe  Glu Asp Arg Lys Asp  Gly Ser Cys Gly Val  Ala Tyr Val
                        2285                2290              2295
```

```
Val Gln  Glu Pro Gly Asp Tyr  Glu Val Ser Val Lys  Phe Asn Glu
                        2300                2305              2310
Glu His  Ile Pro Asp Ser Pro  Phe Val Pro Val  Ala Ser Pro
                        2315                2320              2325
Ser Gly  Asp Ala Arg Arg Leu  Thr Val Ser Ser Leu  Gln Glu Ser
5                       2330                2335              2340
Gly Leu  Lys Val Asn Gln Pro  Ala Ser Phe Ala Val  Ser Leu Asn
                        2345                2350              2355
Gly Ala  Lys Gly Ala Ile Asp  Ala Lys Val His Ser  Pro Ser Gly
10                      2360                2365              2370
Ala Leu  Glu Glu Cys Tyr Val  Thr Glu Ile Asp Gln  Asp Lys Tyr
                        2375                2380              2385
Ala Val  Arg Phe Ile Pro Arg  Glu Asn Gly Val Tyr  Leu Ile Asp
                        2390                2395              2400
Val Lys  Phe Asn Gly Thr His  Ile Pro Gly Ser Pro  Phe Lys Ile
15                      2405                2410              2415
Arg Val  Gly Glu Pro Gly His  Gly Gly Asp Pro Gly  Leu Val Ser
                        2420                2425              2430
Ala Tyr  Gly Ala Gly Leu Glu  Gly Gly Val Thr Gly  Asn Pro Ala
20                      2435                2440              2445
Glu Phe  Val Val Asn Thr Ser  Asn Ala Gly Ala Gly  Ala Leu Ser
                        2450                2455              2460
Val Thr  Ile Asp Gly Pro Ser  Lys Val Lys Met Asp  Cys Gln Glu
                        2465                2470              2475
```

```
Cys Pro Glu Gly Tyr Arg Val  Thr Tyr Thr Pro Met  Ala Pro Gly
     2480                     2485                     2490

Ser Tyr Leu Ile Ser Ile Lys  Tyr Gly Gly Pro Tyr  His Ile Gly
     2495                     2500                     2505

5 Gly Ser Pro Phe Lys Ala Lys  Val Thr Gly Pro Arg  Leu Val Ser
       2510                     2515                     2520

Asn His Ser Leu His Glu Thr   Ser Ser Val Phe Val  Asp Ser Leu
     2525                     2530                     2535

10 Thr Lys Ala Thr Cys Ala Pro  Gln His Gly Ala Pro  Gly Pro Gly
        2540                     2545                     2550

Pro Ala Asp Ala Ser Lys Val   Val Ala Lys Gly Leu  Gly Leu Ser
     2555                     2560                     2565

15 Lys Ala Tyr Val Gly Gln Lys  Ser Ser Phe Thr Val  Asp Cys Ser
        2570                     2575                     2580

Lys Ala Gly Asn Asn Met Leu   Leu Val Gly Val His  Gly Pro Arg
     2585                     2590                     2595

Thr Pro Cys Glu Glu Ile Leu   Val Lys His Val Gly  Ser Arg Leu
     2600                     2605                     2610

20 Tyr Ser Val Ser Tyr Leu Leu  Lys Asp Lys Gly Glu  Tyr Thr Leu
        2615                     2620                     2625

Val Val Lys Trp Gly His Glu   His Ile Pro Gly Ser  Pro Tyr Arg
     2630                     2635                     2640

Val Val Val Pro
     2645
```

```
<210> 10

<211> 199

5 <212> PRT

<213> Homo sapiens

<220>

<221> Transgelin 2

<222> (1)..(199)

10 <223> Accession No. as of 06 Dec 2002: P37802

<400> 10
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```
Met Ala Asn Arg Gly Pro Ala Tyr Gly Leu Ser Arg Glu Val Gln Gln
1               5                   10                  15

Lys Ile Glu Lys Gln Tyr Asp Ala Asp Leu Glu Gln Ile Leu Ile Gln
15          20                  25                  30

Trp Ile Thr Thr Gln Cys Arg Lys Asp Val Gly Arg Pro Gln Pro Gly
        35                  40                  45

Arg Glu Asn Phe Gln Asn Trp Leu Lys Asp Gly Thr Val Leu Cys Glu
20  50                  55                  60

Leu Ile Asn Ala Leu Tyr Pro Glu Gly Gln Ala Pro Val Lys Lys Ile
    65                  70                  75                  80

Gln Ala Ser Thr Met Ala Phe Lys Gln Met Glu Gln Ile Ser Gln Phe
        85                  90                  95
```

<400> 11

```
Met Ala Gly Leu Asn Ser Leu Glu Ala Val Lys Arg Lys Ile Gln Ala
1                   5                   10                  15

Leu Gln Gln Gln Ala Asp Glu Ala Glu Arg Ala Gln Gly Leu Gln
                20                  25                  30

Arg Glu Leu Asp Gly Glu Arg Glu Arg Glu Lys Ala Glu Gly Asp
            35                  40                  45

Val Ala Ala Leu Asn Arg Arg Ile Gln Leu Val Glu Glu Glu Leu Asp
10  50                  55                  60

Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys Leu Glu Glu Ala
65                  70                  75                  80

Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys Val Ile Glu Asn
                85                  90                  95

Arg Ala Met Lys Asp Glu Glu Lys Met Glu Ile Gln Glu Met Gln Leu
15                  100                 105                 110

Lys Glu Ala Lys His Ile Ala Glu Glu Ala Asp Arg Lys Tyr Glu Glu
                    115                 120                 125

Val Ala Arg Lys Leu Val Ile Leu Glu Gly Glu Leu Glu Arg Ala Glu
            130                 135                 140

Glu Arg Ala Glu Val Ser Glu Leu Lys Cys Gly Asp Leu Glu Glu Glu
20  145                 150                 155                 160

Leu Lys Asn Val Thr Asn Asn Leu Lys Ser Leu Glu Ala Ala Ser Glu
            165                 170                 175
```

<210> 11
<211> 248
<212> PRT
<213> Homo sapiens
<220>
<221> Tropomyosin alpha 4 chain
<222> (1)..(248)
<223> Accession No. P07226

```
Leu Gln Ala Ala Glu Arg Tyr Gly Ile Asn Thr Thr Asp Ile Phe Gln
                100                 105                 110

Thr Val Asp Leu Trp Glu Gly Lys Asn Met Ala Cys Val Gln Arg Thr
                115                 120                 125

Leu Met Asn Leu Gly Gly Leu Ala Val Ala Arg Asp Asp Gly Leu Phe
5               130                 135                 140

Ser Gly Asp Pro Asn Trp Phe Pro Lys Ser Lys Glu Asn Pro Arg
            145                 150                 155                 160

Asn Phe Ser Asp Asn Gln Leu Gln Glu Gly Lys Asn Val Ile Gly Leu
10              165                 170                 175

Gln Met Gly Thr Asn Arg Gly Ala Ser Gln Ala Gly Met Thr Gly Tyr
                180                 185                 190

Gly Met Pro Arg Gln Ile Leu
15              195
```

```
Lys Tyr Ser Glu Lys Glu Asp Lys Tyr Glu Glu Glu Ile Lys Leu Leu
                    180             185             190
Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu Phe Ala Glu Arg
                    195             200             205
Thr Val Ala Lys Leu Glu Lys Thr Ile Asp Asp Leu Glu Glu Lys Leu
5                   210             215             220
Ala Gln Ala Lys Glu Glu Asn Val Gly Leu His Gln Thr Leu Asp Gln
                    225             230             235             240
Thr Leu Asn Glu Leu Asn Cys Ile
10                  245


<210> 12
<211> 793
<212> PRT
<213> Homo sapiens
<220>
<221> Caldesmon
<222> (1)..(793)
<223> Accession No. as of 06 Dec 2002: Q05682
<400> 12

Met Asp Asp Phe Glu Arg Arg Arg Glu Leu Arg Arg Gln Lys Arg Glu
1           5               10              15
```

```
Glu Met Arg Leu Glu Ala Glu Arg Ile Ala Tyr Gln Arg Asn Asp Asp
                    20              25              30
Asp Glu Glu Ala Ala Arg Glu Arg Arg Arg Ala Arg Gln Glu
            35              40              45
Arg Leu Arg Gln Lys Gln Glu Glu Glu Ser Leu Gly Gln Val Thr Asp
5           50              55              60
Gln Val Glu Val Asn Ala Gln Asn Ser Val Pro Asp Glu Glu Ala Lys
        65              70              75              80
Thr Thr Thr Asn Thr Gln Val Glu Gly Asp Asp Glu Ala Ala Phe
            85              90              95
Leu Glu Arg Leu Ala Arg Arg Glu Glu Arg Arg Gln Lys Arg Leu Gln
10          100             105             110
Glu Ala Leu Glu Arg Gln Lys Glu Phe Asp Pro Thr Ile Thr Asp Ala
            115             120             125
Ser Leu Ser Leu Pro Ser Arg Arg Met Gln Asn Asp Thr Ala Glu Asn
15          130             135             140
Glu Thr Thr Glu Lys Glu Glu Lys Ser Glu Ser Arg Gln Glu Arg Tyr
            145             150             155             160
Glu Ile Glu Glu Thr Glu Thr Val Thr Lys Ser Tyr Gln Lys Asn Asp
20          165             170             175
Trp Arg Asp Ala Glu Glu Asn Lys Lys Glu Asp Lys Glu Lys Glu Glu
            180             185             190
Glu Glu Glu Lys Pro Lys Arg Gly Ser Ile Gly Glu Asn Gln Val
            195             200             205
```

Glu Val Met Val Glu Glu Lys Thr Thr Glu Ser Gln Glu Thr Val
210   215   220

Val Met Ser Leu Lys Asn Gly Gln Ile Ser Ser Glu Glu Pro Lys Gln
225   230   235   240

5 Glu Glu Arg Glu Gln Gly Ser Asp Glu Ile Ser His His Glu Lys
245   250   255

Met Glu Glu Arg Lys Asp Lys Glu Arg Ala Glu Arg Ala Arg Leu
260   265   270

Glu Ala Glu Glu Arg Glu Arg Ile Lys Ala Glu Gln Asp Lys Ile
10 275   280   285

Ala Asp Glu Arg Arg Ile Glu Ala Glu Lys Glu Ala Ala Ala Gln
290   295   300

Glu Arg Glu Arg Arg Glu Ala Glu Glu Glu Arg Glu Arg Met Arg Glu Glu
305   310   315   320

15 Glu Lys Arg Ala Ala Glu Glu Lys Arg Gln Arg Ile Lys Glu Glu Glu Lys
325   330   335

Arg Ala Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys Arg Ala Ala
340   345   350

Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys Arg Ala Ala Glu
20 355   360   365

Glu Arg Gln Arg Ala Arg Ala Glu Glu Glu Glu Lys Ala Lys Val Glu
370   375   380

Glu Gln Lys Arg Asn Lys Gln Leu Glu Glu Lys Lys Arg Ala Met Gln
385   390   395   400

Glu Thr Lys Ile Lys Gly Glu Glu Lys Val Glu Gln Lys Ile Glu Gly Lys
405   410   415

Trp Val Asn Glu Lys Ala Gln Lys Glu Asp Lys Leu Gln Thr Ala Val
420   425   430

5 Leu Lys Lys Gln Gly Glu Glu Lys Gly Thr Lys Val Gln Ala Lys Arg
435   440   445

Glu Lys Leu Gln Glu Asp Lys Pro Thr Phe Lys Glu Glu Ile Lys
450   455   460

Asp Glu Lys Ile Lys Asp Lys Glu Pro Lys Glu Glu Val Lys Ser
10 465   470   475   480

Phe Met Asp Arg Lys Gly Phe Thr Glu Val Lys Ser Gln Asn Gly
485   490   495

Glu Phe Met Thr His Lys Leu His Thr Glu Asn Thr Phe Ser Arg
500   505   510

15 Pro Gly Gly Arg Ala Ser Val Asp Thr Lys Glu Ala Glu Gly Ala Pro
515   520   525

Gln Val Glu Ala Gly Lys Arg Leu Glu Leu Arg Arg Arg Gly
530   535   540

Glu Thr Glu Ser Glu Glu Phe Glu Lys Leu Lys Gln Lys Gln Glu
20 545   550   555   560

Ala Ala Leu Glu Leu Glu Glu Leu Lys Lys Arg Glu Glu Arg Arg
565   570   575

Lys Val Leu Glu Glu Glu Glu Gln Arg Arg Lys Gln Glu Glu Ala Asp
580   585   590

```
   Arg Lys Leu Arg Glu Glu Glu Lys Arg Arg Leu Lys Glu Glu Ile
            595             600             605

   Glu Arg Arg Ala Glu Ala Ala Glu Lys Arg Gln Lys Met Pro Glu
            610             615             620

 5 Asp Gly Leu Ser Asp Asp Lys Lys Pro Phe Lys Cys Phe Thr Pro Lys
            625             630             635             640

   Gly Ser Ser Leu Lys Ile Glu Glu Arg Ala Glu Phe Leu Asn Lys Ser
            645             650             655

10 Val Gln Lys Ser Ser Gly Val Lys Ser Thr His Gln Ala Ala Ile Val
            660             665             670

   Ser Lys Ile Asp Ser Arg Leu Glu Gln Tyr Thr Ser Ala Ile Glu Gly
            675             680             685

   Thr Lys Ser Ala Lys Pro Thr Lys Pro Ala Ala Ser Asp Leu Pro Val
            690             695             700

15 Pro Ala Glu Gly Val Arg Asn Ile Lys Ser Met Trp Glu Lys Gly Asn
            705             710             715             720

   Val Phe Ser Ser Pro Thr Ala Ala Gly Thr Pro Asn Lys Glu Thr Ala
            725             730             735

   Gly Leu Lys Val Gly Val Ser Ser Arg Ile Asn Glu Trp Leu Thr Lys
            740             745             750

20 Thr Pro Asp Gly Asn Lys Ser Pro Ala Pro Lys Pro Ser Asp Leu Arg
            755             760             765

   Pro Gly Asp Val Ser Ser Lys Ser Arg Asn Leu Trp Glu Lys Gln Ser Val
            770             775             780
```

```
   Asp Lys Val Thr Ser Pro Thr Lys Val
            785             790
```

```
 5 <210> 13
   <211> 458
   <212> PRT
   <213> Homo sapiens
   <220>
10 <221> Alpha enolase
   <222> (1)..(458)
   <223> Accession No. as of 06 Dec 2002: Q05524

   <400> 13

15 Met Ser Ile Leu Lys Ile Ile His Ala Arg Asp Ile Phe Glu Ser Arg
   1               5               10              15

   Gly Asn Pro Thr Val Glu Val Asp Leu Tyr Thr Asn Lys Gly Gly Leu
            20              25              30

   Phe Gly Arg Ala Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu
            35              40              45

20 Ala Leu Leu Glu Leu Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly Gly
            50              55              60

   Lys Gly Val Ser Lys Ala Val Glu His Ile Ile Asn Lys Thr Ile Ala
   65              70              75              80
```

Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro Asp Gln Leu Ala Asp Leu
275   280   285

Tyr Lys Gly Phe Val Leu Gly His Ala Val Lys Asn Tyr Pro Val Gly
290   295   300

5   Val Ser Ile Glu Asp Pro Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp
305   310   315   320

Lys Lys Leu Phe Thr Gly Ser Leu Val Gly Ile Gln Val Val Gly Asp
325   330   335

Asp Leu Thr Val Thr Lys Pro Glu Ala Arg Ile Ala Lys Ala Val Glu
10 340   345   350

Glu Val Lys Ala Cys Asn Cys Leu Leu Leu Lys Val Asn Gln Ile
355   360   365

Gly Ser Val Thr Glu Ser Leu Gln Ala Cys Lys Leu Ala Gln Ser Asn
370   375   380

15 Gly Trp Gly Val Met Pro Val Ser His Arg Leu Ser Gly Glu Thr Glu
385   390   395   400

Asp Thr Phe Met Ala Asp Leu Val Val Gly Leu Cys Thr Gly Gln Ile
405   410   415

Lys Thr Gly Pro Cys Arg Ser Glu Arg Leu Ala Lys Tyr Asn Gln
20 420   425   430

Leu Leu Arg Ile Glu Glu Ala Glu Ala Gly Ser Lys Ala Arg Phe Ala
435   440   445

Gly Arg Asn Phe Arg Asn Pro Arg Ile Asn
450   455

Pro Ala Leu Ile Ser Lys Asn Val Asn Val Val Glu Gln Asp Lys Ile
85   90   95

Asp Asn Leu Met Leu Asp Met Asp Gly Ser Glu Asn Lys Ser Lys Phe
100   105   110

5   Gly Ala Asn Ala Ile Leu Gly Val Ser Leu Ala Val Cys Ser Asn Ala
115   120   125

Gly Ala Thr Ala Glu Lys Gly Val Pro Leu Tyr Arg His Ile Ala Asp
130   135   140

Leu Ala Gly Asn Asn Pro Glu Val Ile Leu Pro Val Pro Ala Phe Asn
10 145   150   155   160

Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu
165   170   175

Phe Met Ile Pro Pro Cys Gly Ala Asp Arg Phe Asn Asp Ala Ile Arg
180   185   190

15 Ile Gly Ala Glu Val Tyr His Asn Leu Lys Asn Val Ile Lys Glu Lys
195   200   205

Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro
210   215   220

Asn Ile Leu Glu Asn Lys Glu Ala Leu Glu Leu Leu Lys Thr Ala Ile
20 225   230   235   240

Gly Lys Ala Gly Tyr Ser Asp Lys Val Val Ile Gly Met Asp Val Ala
245   250   255

Ala Ser Glu Phe Tyr Arg Arg Asp Gly Lys Tyr Asp Leu Asp Phe Asn Ser
260   265   270

```
<210> 14
<211> 408
<212> PRT
<213> Homo sapiens
<220>
<221> Aminoacylase-1
<222> (1)..(408)
<223> Accession No. as of 06 Dec 2002: Q03154
<400> 14

Met Thr Ser Lys Gly Pro Glu Glu Glu His Pro Ser Val Thr Leu Phe
1               5                   10                  15
Arg Gln Tyr Leu Arg Ile Arg Thr Val Gln Pro Lys Pro Asp Tyr Gly
            20                  25                  30
Ala Ala Val Ala Phe Phe Glu Glu Thr Ala Arg Gln Leu Gly Leu Gly
        35                  40                  45
Cys Gln Lys Val Glu Val Ala Pro Gly Tyr Val Val Thr Val Leu Thr
    50                  55                  60
Trp Pro Gly Thr Asn Pro Thr Leu Ser Ser Ile Leu Leu Asn Ser His
65                  70                  75                  80
Thr Asp Val Val Pro Val Phe Lys Glu His Trp Ser His Asp Pro Phe
                85                  90                  95
```

```
Glu Ala Phe Lys Asp Ser Glu Gly Tyr Ile Tyr Ala Arg Gly Ala Gln
                100                 105                 110
Asp Met Lys Cys Val Ser Ile Gln Tyr Leu Glu Ala Val Arg Arg Leu
                115                 120                 125
Lys Val Glu Gly His Arg Phe Pro Arg Thr Ile His Met Thr Phe Val
            130                 135                 140
Pro Asp Glu Glu Val Gly Gly His Gln Gly Met Glu Leu Phe Val Gln
            145                 150                 155                 160
Arg Pro Glu Phe His Ala Leu Arg Ala Gly Phe Ala Leu Asp Glu Gly
                165                 170                 175
Ile Ala Asn Pro Thr Asp Ala Phe Thr Val Phe Tyr Ser Glu Arg Ser
            180                 185                 190
Pro Trp Trp Val Arg Val Thr Ser Thr Gly Arg Pro Gly His Ala Ser
            195                 200                 205
Arg Phe Met Glu Asp Thr Ala Ala Glu Lys Leu His Lys Val Val Asn
            210                 215                 220
Ser Ile Leu Ala Phe Arg Glu Lys Glu Trp Gln Arg Leu Gln Ser Asn
            225                 230                 235                 240
Pro His Leu Lys Glu Gly Ser Val Thr Ser Val Asn Leu Thr Lys Leu
            245                 250                 255
Glu Gly Gly Val Ala Tyr Asn Val Ile Pro Ala Thr Met Ser Ala Ser
            260                 265                 270
Phe Asp Phe Arg Val Ala Pro Asp Val Asp Phe Lys Ala Phe Glu Glu
            275                 280                 285
```

```
Gln Leu Gln Ser Trp Cys Gln Ala Ala Gly Glu Gly Val Thr Leu Glu
              290                 295                 300

Phe Ala Gln Lys Trp Met His Pro Gln Val Thr Pro Asp Asp Ser
              305                 310                 315                 320

Asn Pro Trp Trp Ala Ala Phe Ser Arg Val Cys Lys Asp Met Asn Leu
              325                 330                 335

Thr Leu Glu Pro Glu Ile Met Pro Ala Ala Thr Asp Asn Arg Tyr Ile
              340                 345                 350

Arg Ala Val Gly Val Pro Ala Leu Gly Phe Ser Pro Met Asn Arg Thr
              355                 360                 365

Pro Val Leu His Asp His Asp Glu Arg Leu His Glu Ala Val Phe
              370                 375                 380

Leu Arg Gly Val Asp Ile Tyr Thr Arg Leu Leu Pro Ala Leu Ala Ser
              385                 390                 395                 400

Val Pro Ala Leu Pro Ser Asp Ser
              405
```

```
<210>  15
<211>  277
<212>  PRT
<213>  Homo sapiens
<220>
<221>  F-actin capping protein beta subunit
```

```
<222>  (1)..(277)
<223>  Accession No. as of 06 Dec 2002: P47756
<400>  15
```

```
Met Ser Asp Gln Gln Leu Asp Cys Ala Leu Asp Leu Met Arg Arg Leu
1                  5                  10                 15

Pro Pro Gln Ile Glu Lys Asn Leu Ser Asp Leu Ile Asp Leu Val
              20                 25                 30

Pro Ser Leu Cys Glu Asp Leu Leu Ser Ser Val Asp Gln Pro Leu Lys
              35                 40                 45

Ile Ala Arg Lys Val Val Gly Asp Tyr Leu Leu Cys Asp Tyr
          50                 55                 60

Asn Arg Asp Gly Asp Ser Tyr Arg Ser Pro Trp Ser Asn Lys Tyr Asp
65                 70                 75                 80

Pro Pro Leu Glu Asp Gly Ala Met Pro Ser Ala Arg Leu Arg Lys Leu
              85                 90                 95

Glu Val Glu Ala Asn Asn Ala Phe Asp Gln Tyr Arg Asp Leu Tyr Phe
              100                105                110

Glu Gly Gly Val Ser Ser Val Tyr Leu Trp Asp Leu Asp His Gly Phe
              115                120                125

Ala Gly Val Ile Leu Ile Lys Lys Ala Gly Asp Gly Ser Lys Ile
          130                135                140

Lys Gly Cys Trp Asp Ser Ile His Val Val Glu Val Gln Glu Lys Ser
145                150                155                160
```

Ser Gly Arg Thr Ala His Tyr Lys Leu Thr Ser Thr Val Met Leu Trp
                    165   170   175

Leu Gln Thr Asn Lys Ser Gly Ser Gly Thr Met Asn Leu Gly Gly Ser
            180   185   190

5   Leu Thr Arg Gln Met Glu Lys Asp Glu Thr Val Ser Asp Cys Ser Pro
                        195   200   205

His Ile Ala Asn Ile Gly Arg Leu Val Glu Asp Met Glu Asn Lys Ile
            210   215   220

Arg Ser Thr Leu Asn Glu Ile Tyr Phe Gly Lys Thr Lys Asp Ile Val
            225   230   235   240

10 Asn Gly Leu Arg Ser Ile Asp Ala Ile Pro Asp Asn Gln Lys Phe Lys
                        245   250   255

Gln Leu Gln Arg Glu Leu Ser Gln Val Leu Thr Gln Arg Gln Ile Tyr
                        260   265   270

15 Ile Gln Pro Asp Asn
                275

<210> 16
20 <211> 289
<212> PRT
<213> Homo sapiens

<220>
<221> Inorganic pyrophosphatase

<222> (1)..(289)

<223> Accession No. as of 06 Dec 2002: Q15181

<400> 16

5   Met Ser Gly Phe Ser Thr Glu Glu Arg Ala Ala Pro Phe Ser Leu Glu
1   5   10   15

Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe
            20   25   30

His Asp Ile Pro Ile Tyr Ala Asp Lys Asp Val Phe His Met Val Val
10   35   40   45

Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp
            50   55   60

Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr
65   70   75   80

15 Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala
                        85   90   95

Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly
                        100   105   110

Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys
20   115   120   125

Val Cys Ala Arg Gly Glu Ile Ile Gly Val Lys Val Leu Gly Ile Leu
                        130   135   140

Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn
145   150   155   160

<220>

<221> Galectin-3 (Galactose-specific lectin 3)

<222> (1)..(250)

<223> Accession No. as of 06 Dec 2002: P17931

5   <400> 17

```
Met Ala Asp Asn Phe Ser Leu His Asp Ala Leu Ser Gly Ser Gly Asn
1                   5                   10                  15

Pro Asn Pro Gln Gly Trp Pro Gly Ala Trp Gly Asn Gln Pro Ala Gly
            20                  25                  30

Ala Gly Gly Tyr Pro Gly Ala Ser Tyr Pro Gly Ala Tyr Pro Gly Gln
        35                  40                  45

Ala Pro Pro Gly Ala Tyr Pro Gly Gln Ala Pro Pro Gly Ala Tyr His
    50                  55                  60

Gly Ala Pro Gly Ala Tyr Pro Gly Ala Pro Ala Pro Gly Val Tyr Pro
65                  70                  75                  80

Gly Pro Pro Ser Gly Pro Gly Ala Tyr Pro Ser Ser Gly Gln Pro Ser
                85                  90                  95

Ala Pro Gly Ala Tyr Pro Ala Thr Gly Pro Tyr Gly Ala Pro Ala Gly
            100                 105                 110

Pro Leu Ile Val Pro Tyr Asn Leu Pro Leu Pro Gly Gly Val Val Pro
        115                 120                 125

Arg Met Leu Ile Thr Ile Leu Gly Thr Val Lys Pro Asn Ala Asn Arg
        130                 135                 140
```

```
Val Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys
                165                 170                 175

Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg
                180                 185                 190

Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala
            195                 200                 205

Glu Phe Lys Asp Lys Asp Phe Ala Ile Asp Ile Ile Lys Ser Thr His
        210                 215                 220

Asp His Trp Lys Ala Leu Val Thr Lys Thr Asn Gly Lys Gly Ile
10  225                 230                 235                 240

Ser Cys Met Asn Thr Thr Leu Ser Glu Ser Pro Phe Lys Cys Asp Pro
            245                 250                 255

Asp Ala Ala Arg Ala Ile Val Asp Ala Leu Pro Pro Cys Glu Ser
        260                 265                 270

Ala Cys Thr Val Pro Thr Asp Val Lys Trp Phe His His Gln Lys
15  275                 280                 285

Asn
```

20

<210> 17

<211> 250

<212> PRT

<213> Homo sapiens

```
    Ile Ala Leu Asp Phe Gln Arg Gly Asn Asp Val Ala Phe His Phe Asn
                145                 150                 155             160

    Pro Arg Phe Asn Glu Asn Asn Arg Arg Val Ile Val Cys Asn Thr Lys
                165                 170                 175

 5  Leu Asp Asn Asn Trp Gly Arg Glu Glu Arg Gln Ser Val Phe Pro Phe
                180                 185                 190

    Glu Ser Gly Lys Pro Phe Lys Ile Gln Val Leu Val Glu Pro Asp His
                195                 200                 205

10  Phe Lys Val Ala Val Asn Asp Ala His Leu Leu Gln Tyr Asn His Arg
                210                 215                 220

    Val Lys Lys Leu Asn Glu Ile Ser Lys Leu Gly Ile Ser Gly Asp Ile
                225                 230                 235             240

    Asp Leu Thr Ser Ala Ser Tyr Thr Met Ile
                245                 250

15
```

```
<210> 18
<211> 347
<212> PRT
<213> Homo sapiens
<220>
<221> Voltage-dependent anion-selective channel protein 2 (VDAC-2)
<222> (1)...(347)
<223> Accession No.as of 06 Dec 2002: P45880
```

```
    <400> 18

    Met Ser Trp Cys Asn Glu Leu Arg Leu Pro Ala Leu Lys Gln His Ser
    1               5                   10                  15

    Ile Gly Arg Gly Leu Glu Ser His Ile Thr Met Cys Ile Pro Pro Ser
                20                  25                  30

 5  Tyr Ala Asp Leu Gly Lys Ala Ala Arg Asp Ile Phe Asn Lys Gly Phe
                35                  40                  45

    Gly Phe Gly Leu Val Lys Leu Asp Val Lys Thr Lys Ser Cys Ser Gly
10              50                  55                  60

    Val Glu Phe Ser Thr Ser Gly Ser Ser Asn Thr Asp Thr Gly Lys Val
                65                  70                  75              80

    Thr Gly Thr Leu Glu Thr Lys Tyr Lys Trp Cys Glu Tyr Gly Leu Thr
                85                  90                  95

15  Phe Thr Glu Lys Trp Asn Thr Asp Asn Thr Leu Gly Thr Glu Ile Ala
                100                 105                 110

    Ile Glu Asp Gln Ile Cys Gln Gly Leu Lys Leu Thr Phe Asp Thr Thr
                115                 120                 125

    Phe Ser Pro Asn Thr Gly Lys Lys Ser Gly Lys Ile Lys Ser Ser Tyr
20              130                 135                 140

    Lys Arg Glu Cys Ile Asn Leu Gly Cys Asp Val Asp Phe Asp Phe Ala
                145                 150                 155             160

    Gly Pro Ala Ile His Gly Ser Ala Val Phe Gly Tyr Glu Gly Trp Leu
                165                 170                 175
```

```
     Ala Gly Tyr Gln Met Thr Phe Asp Ser Ala Lys Ser Leu Thr Arg
                     180                 185                 190

     Asn Asn Phe Ala Val Gly Tyr Arg Thr Gly Asp Phe Gln Leu His Thr
                 195                 200                 205

  5  Asn Val Asn Asp Gly Thr Glu Phe Gly Gly Ser Ile Tyr Gln Lys Val
                     210                 215                 220

     Cys Glu Asp Leu Asp Thr Ser Val Asn Leu Ala Trp Thr Ser Gly Thr
                     225                 230                 235            240

     Asn Cys Thr Arg Phe Gly Ile Ala Ala Lys Tyr Gln Leu Asp Pro Thr
 10                  245                 250                 255

     Ala Ser Ile Ser Ala Lys Val Asn Asn Ser Ser Leu Ile Gly Val Gly
                     260                 265                 270

     Tyr Thr Gln Thr Leu Arg Pro Gly Val Lys Leu Thr Leu Ser Ala Leu
 15                  275                 280                 285

     Val Asp Gly Lys Ser Ile Asn Ala Gly Gly His Lys Val Gly Ser Pro
                     290                 295                 300

     Trp Ser Trp Arg Leu Asn Pro Ala Glu Arg Asn Leu Trp Glu Trp Ile
     305                 310                 315                 320

     Ser Glu Asp Leu Ala Leu Ile Tyr Phe His Cys Asp Gln Gln Gln Ala
 20                  325                 330                 335

     Phe Phe Pro Glu Asp Asp Gln Asn Lys Gly
                     340                 345
```

```
     <210> 19
     <211> 339
     <212> PRT
     <213> Homo sapiens

  5  <220>
     <221> Annexin II
     <222> (1)..(339)
     <223> Accession No. as of 06 Dec 2002: P07355

 10  <400> 19

     Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp
     1               5                   10                  15

     His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn
                     20                  25                  30

 15  Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr
                     35                  40                  45

     Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser
                     50                  55                  60

     Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys
 20  65                  70                  75                  80

     Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu
                     85                  90                  95

     Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser
                     100                 105                 110
```

```
Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu
            115                 120                 125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn
            130                 135                 140

5   Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile
            145                 150                 155             160

Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys
            165                 170                 175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp
10          180                 185                 190

Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr
            195                 200                 205

Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His
            210                 215                 220

Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met
15          225                 230                 235             240

Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe
            245                 250                 255

Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp
            260                 265                 270

Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu
20          275                 280                 285

Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg
            290                 295                 300
```

```
Ser Glu Phe Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln
            305                 310                 315             320

Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly
            325                 330                 335

5   Gly Asp Asp


10  <210> 20
    <211> 418
    <212> PRT
    <213> Homo sapiens
    <220>
    <221> Collagen-binding protein 2 precursor
15  <222> (1)..(418)
    <223> Accession No. as of 06 Dec 2002: P50454
    <400> 20

Met Arg Ser Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
20  1               5                   10                  15

Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
                20                  25                  30

Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala
                35                  40                  45
```

```
Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val
                    50                  55                  60

Glu Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu
65                  70                  75                  80

Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val
                    85                  90                  95

Leu Ser Ala Glu Gln Leu Arg Asp Glu Val His Ala Gly Leu Gly
                    100                 105                 110

Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp
            115                 120                 125

Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp
            130                 135                 140

Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys
145                 150                 155                 160

Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp
                    165                 170                 175

Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val
                    180                 185                 190

Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro
            195                 200                 205

His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe
            210                 215                 220

Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met His Arg Thr
225                 230                 235                 240
```

```
Gly Leu Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val
                    245                 250                 255

Glu Met Pro Leu Ala His Lys Leu Ser Ser Ile Ile Leu Met Pro
                    260                 265                 270

His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu
5                   275                 280                 285

Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile
                    290                 295                 300

Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His
10  305                 310                 315                 320

Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp
                    325                 330                 335

Leu Ser Arg Met Ser Gly Lys Asp Leu Tyr Leu Ala Ser Val Phe
                    340                 345                 350

His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln
15                  355                 360                 365

Asp Ile Tyr Gly Arg Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala
                    370                 375                 380

Asp His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu
20  385                 390                 395                 400

Leu Phe Ile Gly Arg Leu Val Arg Pro Lys Gly Asp Lys Met Arg Asp
                    405                 410                 415

Glu Leu
```

```
      <210> 21
      <211> 166
      <212> PRT
      <213> Homo sapiens
      <220>
      <221> Cofilin, non-muscle isoform
      <222> (1)..(166)
  10  <223> Accession No. as of 08 ec 2002: P23528
      <400> 21

      Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe Asn
  1                5                      10                      15
  15  Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys Arg
                      20                      25                      30
      Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile Ile
                      35                      40                      45
      Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr Val
  20      50                      55                      60
      Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp Cys
  65                      70                      75                      80
      Arg Tyr Ala Leu Tyr Asp Ala Thr Tyr Glu Thr Lys Glu Ser Lys Lys
                      85                      90                      95
```

```
      Glu Asp Leu Val Phe Ile Phe Trp Ala Pro Glu Ser Ala Pro Leu Lys
                      100                     105                     110
      Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Leu
                      115                     120                     125
  5   Thr Gly Ile Lys His Glu Leu Gln Ala Asn Cys Tyr Glu Glu Val Lys
                      130                     135                     140
      Asp Arg Cys Thr Leu Ala Glu Lys Leu Gly Gly Ser Ala Val Ile Ser
      145                     150                     155                     160
      Leu Glu Gly Lys Pro Leu
  10

      <210> 22
      <211> 165
  15  <212> PRT
      <213> Homo sapiens
      <220>
      <221> Peptidyl-prolyl cis-trans isomerase A
      <222> (1)..(165)
  20  <223> Accession No. as of 09 Dec 2002: P05092

      <400> 22

      Met Val Asn Pro Thr Val Phe Phe Asp Ile Ala Val Asp Gly Glu Pro
  1                5                      10                      15
```

```
     Leu Gly Arg Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro Lys Thr
                     20                  25                  30

     Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Phe Gly Tyr
                     35                  40                  45

  5  Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln Gly
                     50                  55                  60

     Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys Ser Ile Tyr Gly
     65                  70                  75                  80

 10  Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His Thr Gly Pro Gly
                     85                  90                  95

     Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe
                     100                 105                 110

     Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly Lys His Val Val
                     115                 120                 125

 15  Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu Ala Met Glu Arg
                     130                 135                 140

     Phe Gly Ser Arg Asn Gly Lys Thr Ser Lys Ile Thr Ile Ala Asp
     145                 150                 155                 160

     Cys Gly Gln Leu Glu
                     165
 20
```

<210> 23
<211> 638

```
     <212> PRT

     <213> Homo sapiens

     <220>

     <221> Dynein intermediate chain 2, cytosolic

  5  <222> (1)..(638)

     <223> Accession No. as of 09 Dec 2002: Q13409

     <400> 23


     Met Ser Asp Lys Ser Glu Leu Lys Ala Glu Leu Glu Arg Lys Lys Gln
 10  1               5                   10                  15

     Arg Leu Ala Gln Ile Arg Glu Glu Lys Lys Arg Lys Glu Glu Glu Arg
                     20                  25                  30

     Lys Lys Glu Thr Asp Gln Lys Lys Glu Ala Val Ala Pro Val Gln
 15  35                  40                  45

     Glu Glu Ser Asp Leu Glu Lys Lys Arg Arg Glu Ala Glu Ala Leu Leu
                     50                  55                  60

     Gln Ser Met Gly Leu Thr Pro Glu Ser Pro Ile Val Phe Ser Glu Tyr
     65                  70                  75                  80

     Trp Val Pro Pro Met Ser Pro Ser Ser Val Ser Thr Pro
 20                  85                  90                  95

     Ser Glu Ala Gly Ser Gln Asp Ser Gly Asp Gly Ala Val Gly Ser Arg
                     100                 105                 110

     Thr Leu His Trp Asp Thr Asp Pro Ser Val Leu Gln Leu His Ser Asp
     115                 120                 125
```

Ser Asp Leu Gly Arg Gly Pro Ile Lys Leu Gly Met Ala Lys Ile Thr
130   135   140

Gln Val Asp Phe Pro Pro Arg Glu Ile Val Thr Tyr Thr Lys Glu Thr
145   150   155   160

Gln Thr Pro Val Met Ala Gln Lys Pro Glu Asp Glu Glu Asp Asp
5   165   170   175

Asp Val Val Ala Pro Lys Pro Pro Ile Glu Pro Glu Glu Lys Thr
180   185   190

Leu Lys Lys Asp Glu Glu Asn Asp Ser Lys Ala Pro Pro His Glu Leu
10   195   200   205

Thr Glu Glu Lys Gln Gln Ile Leu His Ser Glu Glu Phe Leu Ser
210   215   220

Phe Phe Asp His Ser Thr Arg Ile Val Glu Arg Ala Leu Ser Glu Gln
15   225   230   235   240

Ile Asn Ile Phe Phe Asp Tyr Ser Gly Arg Asp Leu Glu Asp Lys Glu
245   250   255

Gly Glu Ile Gln Ala Gly Ala Lys Leu Ser Leu Asn Arg Gln Phe Phe
260   265   270

Asp Glu Arg Trp Ser Lys Val Val Ser Cys Leu Asp Trp Ser
20   275   280   285

Ser Gln Tyr Pro Glu Leu Leu Val Ala Ser Tyr Asn Asn Asn Glu Asp
290   295   300

Ala Pro His Glu Pro Asp Gly Val Ala Leu Val Trp Asn Met Lys Tyr
305   310   315   320

Lys Lys Thr Thr Pro Glu Tyr Val Phe His Cys Gln Ser Ala Val Met
325   330   335

Ser Ala Thr Phe Ala Lys His Pro Asn Leu Val Val Gly Gly Thr
340   345   350

Tyr Ser Gly Gln Ile Val Leu Trp Asp Asn Arg Ser Asn Lys Arg Thr
5   355   360   365

Pro Val Gln Arg Thr Pro Leu Ser Ala Ala His His His Pro Val
370   375   380

Tyr Cys Val Asn Val Val Gly Thr Gln Asn Ala His Asn Leu Ile Ser
10 385   390   395   400

Ile Ser Thr Asp Gly Lys Ile Cys Ser Trp Ser Asp Met Leu Ser
405   410   415

His Pro Gln Asp Ser Met Glu Leu Val His Lys Gln Ser Lys Ala Val
420   425   430

Ala Val Thr Ser Met Ser Phe Pro Val Gly Asp Val Asn Asn Phe Val
15 435   440   445

Val Gly Ser Glu Glu Gly Ser Val Tyr Thr Ala Cys Arg His Gly Ser
450   455   460

Lys Ala Gly Ile Ser Glu Met Phe Glu Gly His Gln Gly Pro Ile Thr
20 465   470   475   480

Gly Ile His Cys His Ala Ala Val Gly Ala Val Asp Phe Ser His Leu
485   490   495

Phe Val Thr Ser Ser Phe Asp Trp Thr Val Lys Leu Trp Thr Thr Lys
500   505   510

```
Asn Asn Lys Pro Leu Tyr Ser Phe Glu Asp Asn Ala Asp Tyr Val Tyr
                  515                 520                 525

Asp Val Met Trp Ser Pro Thr His Pro Ala Leu Phe Ala Cys Val Asp
                  530                 535                 540

  5  Gly Met Gly Arg Leu Asp Leu Trp Asn Leu Asn Asn Asp Thr Glu Val
      545                 550                 555                 560

Pro Thr Ala Ser Ile Ser Val Glu Gly Asn Pro Ala Leu Asn Arg Val
                  565                 570                 575

Arg Trp Thr His Ser Gly Arg Glu Ile Ala Val Gly Asp Ser Glu Gly
 10               580                 585                 590

Gln Ile Val Ile Tyr Asp Val Gly Glu Gln Ile Ala Val Pro Arg Asn
                  595                 600                 605

Asp Glu Trp Ala Arg Phe Gly Arg Thr Leu Ala Glu Ile Asn Ala Asn
                  610                 615                 620

 15  Arg Ala Asp Ala Glu Glu Ala Ala Thr Arg Ile Pro Ala
      625                 630                 635


<210> 24
<211> 328
<212> PRT
<213> Homo sapiens
<220>
<221> Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor
```

```
<222> (1)..(328)

<223> Accession No. as of 09 Dec 2002: Q13011

<400> 24

  5  Met Ala Ala Gly Ile Val Ala Ser Arg Arg Asp Leu Leu Thr
      1                 5                   10                  15

Arg Arg Leu Thr Gly Ser Asn Tyr Pro Gly Leu Ser Ile Ser Leu Arg
                  20                  25                  30

Leu Thr Gly Ser Ser Ala Gln Glu Glu Ala Ser Gly Val Ala Leu Gly
 10               35                  40                  45

Glu Ala Pro Asp His Ser Tyr Glu Ser Leu Arg Val Thr Ser Ala Gln
                  50                  55                  60

Lys His Val Leu His Val Gln Leu Asn Arg Pro Asn Lys Arg Asn Ala
 65               70                  75                  80

 15  Met Asn Lys Val Phe Trp Arg Glu Met Val Glu Cys Phe Asn Lys Ile
                  85                  90                  95

Ser Arg Asp Ala Asp Cys Arg Ala Val Val Ile Ser Gly Ala Gly Lys
                  100                 105                 110

Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu
 20               115                 120                 125

Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp
                  130                 135                 140

Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg Cys Pro
145               150                 155                 160
```

```
Lys Pro Val Ile Ala Ala His Gly Cys Ile Gly Gly Val
            165                 170                 175

Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp Ala Phe
        180                 185                 190

Phe Gln Val Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val Gly Thr
5               195                 200                 205

Leu Glu Arg Leu Pro Lys Val Ile Gly Asn Gln Ser Leu Val Asn Glu
        210                 215                 220

Leu Ala Phe Thr Ala His Lys Met Met Ala Asp Glu Ala Leu Asp Ser
10  225                 230                 235                 240

Gly Leu Val Ser Arg Val Phe Pro Asp Lys Glu Val Met Leu Asp Ala
            245                 250                 255

Ala Leu Pro Leu Ala Pro Glu Ile Ser Ser Lys Thr Thr Val Leu Val
        260                 265                 270

Gln Ser Thr Lys Val Asn Leu Leu Tyr Ser Arg Asp His Ser Val Ala
15  275                 280                 285

Glu Ser Leu Asn Tyr Val Ala Ser Trp Asn Met Ser Met Leu Gln Thr
        290                 295                 300

Gln Asp Leu Val Lys Ser Val Gln Pro Thr Thr Glu Asn Lys Glu Leu
20  305                 310                 315                 320

Lys Thr Val Thr Phe Ser Lys Leu
    325
```

```
<210> 25
<211> 1657
<212> PRT
<213> Homo sapiens

<220>
<221> Ras GTPase-activating-like protein IQGAP1
<222> (1)..(1657)
<223> Accession No. as of 09 Dec 2002: P46940

<400> 25

Met Ser Ala Ala Asp Glu Val Asp Gly Leu Gly Val Ala Arg Pro His
1               5                   10                  15

Tyr Gly Ser Val Leu Asp Asn Glu Arg Leu Thr Ala Glu Glu Met Asp
            20                  25                  30

Glu Arg Arg Gln Asn Val Ala Tyr Glu Tyr Leu Cys His Leu Glu
        35                  40                  45

Glu Ala Lys Arg Trp Met Glu Ala Cys Leu Gly Glu Asp Leu Pro Pro
        50                  55                  60

Thr Thr Glu Leu Glu Glu Gly Leu Arg Asn Gly Val Tyr Leu Ala Lys
65                  70                  75                  80

Leu Gly Asn Phe Phe Ser Pro Lys Val Val Ser Leu Lys Lys Ile Tyr
                85                  90                  95

Asp Arg Glu Gln Thr Arg Tyr Lys Ala Thr Gly Leu His Phe Arg His
            100                 105                 110
```

Thr Asp Asn Val Ile Gln Trp Leu Asn Ala Met Asp Glu Ile Gly Leu
115   120   125

Pro Lys Ile Phe Tyr Pro Glu Thr Asp Ile Tyr Asp Arg Lys Asn
130   135   140

Met Pro Arg Cys Ile Tyr Cys Ile His Ala Leu Ser Leu Tyr Leu Phe
5   145   150   155   160

Lys Leu Gly Leu Ala Pro Gln Ile Gln Asp Leu Tyr Gly Lys Val Asp
165   170   175

Phe Thr Glu Glu Ile Asn Asn Met Lys Thr Glu Leu Glu Lys Tyr
180   185   190

10

Gly Ile Gln Met Pro Ala Phe Ser Lys Ile Gly Gly Ile Leu Ala Asn
195   200   205

Glu Leu Ser Val Asp Glu Ala Ala Leu His Ala Ala Val Ile Ala Ile
210   215   220

15 Asn Glu Ala Ile Asp Arg Ile Pro Ala Asp Thr Phe Ala Ala Leu
225   230   235   240

Lys Asn Pro Asn Ala Met Leu Val Asn Leu Glu Glu Pro Leu Ala Ser
245   250   255

Thr Tyr Gln Asp Ile Leu Tyr Gln Ala Lys Gln Asp Lys Met Thr Asn
20   260   265   270

Ala Lys Asn Arg Thr Glu Asn Ser Glu Arg Glu Arg Asp Val Tyr Glu
275   280   285

Glu Leu Leu Thr Gln Ala Glu Ile Gln Gly Asn Ile Asn Lys Val Asn
290   295   300

Thr Phe Ser Ala Leu Ala Asn Ile Asp Leu Ala Leu Glu Gln Gly Asp
305   310   315   320

Ala Leu Ala Leu Phe Arg Ala Leu Gln Ser Ala Leu Gly Leu Arg
325   330   335

5 Gly Leu Gln Gln Asn Ser Asp Trp Tyr Leu Lys Gln Leu Leu Ser
340   345   350

Asp Lys Gln Gln Lys Arg Gln Ser Gly Gln Thr Asp Pro Leu Gln Lys
355   360   365

Glu Glu Gln Ser Gly Val Asp Ala Ala Asn Ser Ala Ala Gln Gln
10   370   375   380

Tyr Gln Arg Arg Leu Ala Ala Val Ala Leu Ile Asn Ala Ala Ile Gln
385   390   395   400

Lys Gly Val Ala Glu Lys Thr Val Leu Glu Leu Met Asn Pro Glu Ala
405   410   415

15 Gln Leu Pro Gln Val Tyr Pro Phe Ala Ala Asp Leu Tyr Gln Lys Glu
420   425   430

Leu Ala Thr Leu Gln Arg Gln Ser Pro Glu His Asn Leu Thr His Pro
435   440   445

Glu Leu Ser Val Ala Val Glu Met Leu Ser Ser Val Ala Leu Ile Asn
450   455   460

20 Arg Ala Leu Glu Ser Gly Asp Val Asn Thr Val Trp Lys Gln Leu Ser
465   470   475   480

Ser Ser Val Thr Gly Leu Thr Asn Ile Glu Glu Glu Asn Cys Gln Arg
485   490   495

Tyr Leu Asp Glu Leu Met Lys Leu Lys Ala Gln Ala His Ala Ala Glu Asn
500   505   510

Asn Glu Phe Ile Thr Trp Asn Asp Ile Gln Ala Cys Val Asp His Val
515   520   525

5   Asn Leu Val Val Gln Glu Glu His Glu Arg Ile Leu Ala Ile Gly Leu
530   535   540

Ile Asn Glu Ala Leu Asp Glu Gly Asp Ala Gln Lys Thr Leu Gln Ala
545   550   555   560

Leu Gln Ile Pro Ala Ala Lys Leu Glu Gly Val Leu Ala Glu Val Ala
10   565   570   575

Gln His Tyr Gln Asp Thr Leu Ile Arg Ala Lys Arg Glu Lys Ala Gln
580   585   590

Glu Ile Gln Asp Glu Ser Ala Val Leu Trp Leu Asp Glu Ile Gln Gly
595   600   605

Gly Ile Trp Gln Ser Asn Lys Asp Thr Gln Glu Ala Gln Lys Phe Ala
15   610   615   620

Leu Gly Ile Phe Ala Ile Asn Glu Ala Val Glu Ser Gly Asp Val Gly
625   630   635   640

Lys Thr Leu Ser Ala Leu Arg Ser Pro Asp Val Gly Leu Tyr Gly Val
645   650   655

Ile Pro Glu Cys Gly Glu Thr Tyr His Ser Asp Leu Ala Glu Ala Lys
20   660   665   670

Lys Lys Lys Ala Val Gly Asp Asn Asn Ser Lys Trp Val Lys His
675   680   685

Trp Val Lys Gly Gly Tyr Tyr Tyr His Asn Leu Glu Thr Gln Glu
690   695   700

Gly Gly Trp Asp Glu Pro Asn Phe Val Gln Asn Ser Met Gln Leu
705   710   715   720

5   Ser Ser Arg Glu Glu Ile Gln Ser Ser Ile Ser Gly Val Thr Ala Ala Tyr
725   730   735

Asn Asn Arg Glu Gln Leu Trp Leu Ala Asn Glu Gly Leu Ile Thr Arg Leu
740   745   750

Gln Ala Arg Cys Arg Gly Tyr Leu Val Arg Gln Glu Phe Arg Ser Arg
10   755   760   765

Met Asn Phe Leu Lys Gln Ile Pro Ala Ile Thr Cys Ile Gln Ser
770   775   780

Gln Trp Arg Gly Tyr Lys Gln Lys Lys Ala Tyr Gln Asp Arg Leu Ala
785   790   795   800

15 Tyr Leu Arg Ser His Lys Asp Glu Val Val Lys Ile Gln Ser Leu Ala
805   810   815

Arg Met His Gln Ala Arg Lys Arg Tyr Arg Asp Arg Leu Gln Tyr Phe
820   825   830

Arg Asp His Ile Asn Asp Ile Ile Lys Ile Gln Ala Phe Ile Arg Ala
835   840   845

20 Asn Lys Ala Arg Asp Asp Tyr Lys Thr Leu Ile Asn Ala Glu Asp Pro
850   855   860

Pro Met Val Val Val Arg Lys Phe Val His Leu Leu Asp Gln Ser Asp
865   870   875   880

```
    Gln Asp Phe Gln Glu Leu Asp Leu Met Lys Met Arg Glu Glu Val
                885             890             895
    Ile Thr Leu Ile Arg Ser Asn Gln Gln Leu Glu Asn Asp Leu Asn Leu
                900             905             910
5   Met Asp Ile Lys Ile Gly Leu Leu Val Lys Asn Lys Ile Thr Leu Gln
                915             920             925
    Asp Val Val Ser His Ser Lys Lys Leu Thr Lys Lys Asn Lys Glu Gln
                930             935             940
    Leu Ser Asp Met Met Met Ile Asn Lys Gln Lys Gly Gly Leu Lys Ala
10  945             950             955             960
    Leu Ser Lys Glu Lys Arg Glu Lys Leu Glu Ala Tyr Gln His Leu Phe
                965             970             975
    Tyr Leu Leu Gln Thr Asn Pro Thr Tyr Leu Ala Lys Leu Ile Phe Gln
                980             985             990
15  Met Pro Gln Asn Lys Ser Thr Lys Phe Met Asp Ser Val Ile Phe Thr
                995             1000            1005
    Leu Tyr Asn Tyr Ala Ser Asn Gln Arg Glu Glu Tyr Leu Leu Leu
                1010            1015            1020
    Arg Leu Phe Lys Thr Ala Leu Gln Glu Glu Ile Glu Lys Ser Lys Val
                1025            1030            1035
20  Asp Gln Ile Gln Glu Ile Val Thr Gly Asn Pro Thr Val Ile Lys
                1040            1045            1050
    Met Val Val Ser Phe Asn Arg Gly Ala Arg Gly Gln Asn Ala Leu
                1055            1060            1065
```

```
    Arg Gln Ile Leu Ala Pro Val Val Lys Glu Ile Met Asp Asp Lys
                1070            1075            1080
    Ser Leu Asn Ile Lys Thr Asp Pro Val Asp Ile Tyr Lys Ser Trp
                1085            1090            1095
5   Val Asn Gln Met Glu Ser Gln Thr Gly Glu Ala Ser Lys Leu Pro
                1100            1105            1110
    Tyr Asp Val Thr Pro Glu Gln Ala Leu Ala Ala His Glu Glu Val Lys
                1115            1120            1125
    Thr Arg Leu Asp Ser Ser Ile Arg Asn Met Arg Ala Val Thr Asp
10              1130            1135            1140
    Lys Phe Leu Ser Ala Ile Val Ser Ser Val Asp Lys Ile Pro Tyr
                1145            1150            1155
    Gly Met Arg Phe Ile Ala Lys Val Leu Lys Asp Ser Leu His Glu
                1160            1165            1170
15  Lys Phe Pro Asp Ala Gly Glu Asp Glu Leu Leu Lys Ile Ile Gly
                1175            1180            1185
    Asn Leu Leu Tyr Tyr Arg Tyr Met Asn Pro Ala Ile Val Ala Pro
                1190            1195            1200
    Asp Ala Phe Asp Ile Ile Asp Leu Ser Ala Gly Gly Gln Leu Thr
20  1205            1210            1215
    Thr Asp Gln Arg Arg Asn Leu Gly Ser Ile Ala Lys Met Leu Gln
                1220            1225            1230
    His Ala Ala Ser Asn Lys Met Phe Leu Gly Asp Asn Ala His Leu
                1235            1240            1245
```

```
Ser Ile Ile Asn Glu Tyr Leu Ser Gln Ser Tyr Gln Lys Phe Arg
                1250                    1255                    1260

Arg Phe Phe Gln Thr Ala Cys Asp Val Pro Glu Leu Gln Asp Lys
                1265                    1270                    1275

5   Phe Asn Val Asp Glu Tyr Ser Asp Leu Val Thr Leu Thr Lys Pro
                1280                    1285                    1290

    Val Ile Tyr Ile Ser Ile Gly Glu Ile Ile Asn Thr His Thr Leu
                1295                    1300                    1305

    Leu Leu Asp His Gln Asp Ala Ile Ala Pro Glu His Asn Asp Pro
10              1310                    1315                    1320

    Ile His Glu Leu Leu Asp Asp Leu Gly Glu Val Pro Thr Ile Glu
                1325                    1330                    1335

    Ser Leu Ile Gly Glu Ser Ser Gly Asn Leu Asn Asp Pro Asn Lys
                1340                    1345                    1350

15  Glu Ala Leu Ala Lys Thr Glu Val Ser Leu Thr Leu Thr Asn Lys
                1355                    1360                    1365

    Phe Asp Val Pro Gly Asp Glu Asn Ala Glu Met Asp Ala Arg Thr
                1370                    1375                    1380

    Ile Leu Leu Asn Thr Lys Arg Leu Ile Val Asp Val Ile Arg Phe
20              1385                    1390                    1395

    Gln Pro Gly Glu Thr Leu Thr Glu Ile Leu Glu Thr Pro Ala Thr
                1400                    1405                    1410

    Ser Glu Gln Glu Ala Glu His Gln Arg Ala Met Gln Arg Arg Ala
                1415                    1420                    1425
```

```
Ile Arg Asp Ala Lys Thr Pro Asp Lys Met Lys Lys Ser Lys Ser
                1430                    1435                    1440

Val Lys Glu Asp Ser Asn Leu Thr Leu Gln Glu Lys Lys Glu Lys
                1445                    1450                    1455

5   Ile Gln Thr Gly Leu Lys Lys Leu Thr Glu Leu Gly Thr Val Asp
                1460                    1465                    1470

    Pro Lys Asn Lys Tyr Gln Glu Leu Ile Asn Asp Ile Ala Arg Asp
                1475                    1480                    1485

    Ile Arg Asn Gln Arg Arg Tyr Arg Gln Arg Arg Lys Ala Glu Leu
10              1490                    1495                    1500

    Val Lys Leu Gln Gln Thr Tyr Ala Ala Leu Asn Ser Lys Ala Thr
                1505                    1510                    1515

    Phe Tyr Gly Glu Gln Val Asp Tyr Tyr Lys Ser Tyr Ile Lys Thr
                1520                    1525                    1530

15  Cys Leu Asp Asn Leu Ala Ser Lys Gly Lys Val Ser Lys Lys Pro
                1535                    1540                    1545

    Arg Glu Met Lys Gly Lys Lys Ser Lys Lys Ile Ser Leu Lys Tyr
                1550                    1555                    1560

    Thr Ala Ala Arg Leu His Glu Lys Gly Val Leu Leu Glu Ile Glu
20              1565                    1570                    1575

    Asp Leu Gln Val Asn Gln Phe Lys Asn Val Ile Phe Glu Ile Ser
                1580                    1585                    1590

    Pro Thr Glu Glu Val Gly Asp Phe Glu Val Lys Ala Lys Phe Met
                1595                    1600                    1605
```

```
Gly Val Gln Met Glu Thr Phe Met Leu His Tyr Gln Asp Leu Leu
        1610            1615            1620

Gln Leu Gln Tyr Glu Gly Val Ala Val Met Lys Leu Phe Asp Arg
        1625            1630            1635

Ala Lys Val Asn Val Asn Leu Leu Ile Phe Leu Leu Asn Lys Lys
        1640            1645            1650

Phe Tyr Gly Lys
        1655
```

<210> 26
<211> 627
<212> PRT
<213> Homo sapiens
<220>
<221> L-plastin (Lymphocyte cytosolic protein 1)
<222> (1)..(627)
<223> Accession No. as of 09 Dec 2002: P13796
<400> 26

```
Met Ala Arg Gly Ser Val Ser Asp Glu Glu Met Met Glu Leu Arg Glu
1                   5                   10                  15

Ala Phe Ala Lys Val Asp Thr Asp Gly Asn Gly Tyr Ile Ser Phe Asn
```

```
                    20                  25                  30
Glu Leu Asn Asp Leu Phe Lys Ala Ala Cys Leu Pro Leu Pro Gly Tyr
                    35                  40                  45
Arg Val Arg Glu Ile Thr Glu Asn Leu Met Ala Thr Gly Asp Leu Asp
5                   50                  55                  60
Gln Asp Gly Arg Ile Ser Phe Asp Glu Phe Ile Lys Ile Phe His Gly
                    65                  70                  75                  80
Leu Lys Ser Thr Asp Val Ala Lys Thr Phe Arg Lys Ala Ile Asn Lys
                    85                  90                  95
10  Lys Glu Gly Ile Cys Ala Ile Gly Gly Thr Ser Glu Gln Ser Ser Val
                    100                 105                 110
Gly Thr Gln His Ser Tyr Ser Glu Glu Glu Lys Tyr Ala Phe Val Asn
                    115                 120                 125
Trp Ile Asn Lys Ala Leu Glu Asn Asp Pro Asp Cys Arg His Val Ile
15                  130                 135                 140
Pro Met Asn Pro Asn Thr Asn Asp Leu Phe Asn Ala Val Gly Asp Gly
145                 150                 155                 160
Ile Val Leu Cys Lys Met Ile Asn Leu Ser Val Pro Asp Thr Ile Asp
                    165                 170                 175
20  Glu Arg Thr Ile Asn Lys Lys Lys Leu Thr Pro Phe Thr Ile Gln Glu
                    180                 185                 190
Asn Leu Asn Leu Ala Leu Asn Ser Ala Ser Ala Ile Gly Cys His Val
                    195                 200                 205
Val Asn Ile Gly Ala Glu Asp Leu Lys Glu Gly Lys Pro Tyr Leu Val
```

Leu Gly Leu Leu Trp Gln Val Ile Lys Ile Gly Leu Phe Ala Asp Ile
210   215   220
     225   230   235   240

Glu Leu Ser Arg Asn Glu Ala Leu Ile Ala Leu Arg Glu Arg Gly Glu
5   245   250   255

Ser Leu Glu Asp Leu Met Lys Leu Ser Pro Glu Glu Leu Leu Arg
260   265   270

Trp Ala Asn Tyr His Leu Glu Asn Ala Gly Cys Asn Lys Ile Gly Asn
275   280   285

10 Phe Ser Thr Asp Ile Lys Asp Ser Lys Ala Tyr Tyr His Leu Leu Glu
290   295   300

Gln Val Ala Pro Lys Gly Asp Glu Glu Gly Val Pro Ala Val Val Ile
305   310   315   320

Asp Met Ser Gly Leu Arg Glu Lys Asp Asp Ile Gln Arg Ala Glu Cys
15   325   330   335

Met Leu Gln Gln Ala Glu Arg Leu Gly Cys Arg Gln Phe Val Thr Ala
340   345   350

Thr Asp Val Val Arg Gly Asn Pro Lys Leu Asn Leu Ala Phe Ile Ala
355   360   365

20 Asn Leu Phe Asn Arg Tyr Pro Ala Leu His Lys Pro Glu Asn Gln Asp
370   375   380

Ile Asp Trp Gly Ala Leu Glu Gly Glu Thr Arg Glu Arg Thr Phe
385   390   395   400

Arg Asn Trp Met Asn Ser Leu Gly Val Asn Pro Arg Val Asn His Leu

---

Tyr Ser Asp Ser Asp Ala Leu Val Ile Phe Gln Leu Tyr Glu Lys
405   410   415
     420   425   430

Ile Lys Val Pro Val Asp Trp Asn Arg Val Asn Lys Pro Tyr Pro
435   440   445

5 Lys Leu Gly Gly Asn Met Lys Leu Lys Leu Glu Asn Cys Asn Tyr Ala Val
450   455   460

Glu Leu Gly Lys Asn Gln Ala Lys Phe Ser Leu Val Gly Ile Gly Gly
465   470   475   480

10 Gln Asp Leu Asn Glu Gly Asn Arg Thr Leu Asn Ile Leu Ala Leu Ile Trp
485   490   495

Gln Leu Met Arg Arg Tyr Thr Leu Asn Ile Leu Glu Glu Ile Gly Gly Gly
500   505   510

Gly Gln Lys Val Asn Asp Asp Ile Ile Val Asn Trp Val Asn Glu Thr
15   515   520   525

Leu Arg Glu Ala Glu Lys Ser Ser Ser Ile Ser Ser Phe Lys Asp Pro
530   535   540

Lys Ile Ser Thr Ser Leu Pro Val Leu Asp Leu Ile Asp Ala Ile Gln
545   550   555   560

20 Pro Gly Ser Ile Asn Tyr Asp Leu Leu Lys Thr Glu Asn Leu Asn Asp
565   570   575

Asp Glu Lys Leu Asn Asn Ala Lys Tyr Ala Ile Ser Met Ala Arg Lys
580   585   590

Ile Gly Ala Arg Val Tyr Ala Leu Pro Glu Asp Leu Val Glu Val Asn

```
                    50              55              60
   Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Arg Gly Tyr Tyr

                       65              70              75              80
   Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val

                       85              90              95
5  Thr Tyr Lys Asn Val Pro Asn Trp His Arg Arg Asp Leu Val Arg Val Cys

                      100             105             110
   Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp

                      115             120             125
10 Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu

                      130             135             140
   Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro

                      145             150             155             160
   Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe

15                    165             170             175
   Val Ala Met Pro Ala Leu Ala Pro Glu Val Val Met Asp Pro Ala

                      180             185             190
   Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala

                      195             200             205
20 Leu Pro Asp Glu Asp Asp Leu

                      210             215
```

<210> 28

```
                    595             600             605
   Pro Lys Met Val Met Thr Val Phe Ala Cys Leu Met Gly Lys Gly Met

                      610             615             620
   Lys Arg Val

5  625
```

<210> 27
<211> 216
<212> PRT
<213> Homo sapiens
<220>
<221> GTP-binding nuclear protein RAN
<222> (1)..(216)
<223> Accession No. as of 09 Dec 2002: P17080
<400> 27

```
   1                   5               10              15
   Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val

                       20              25              30
20 Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr

                       35              40              45
   Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His

   Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
```

```
<211>  463
<212>  PRT
<213>  Homo sapiens
<220>
<221>  Heterogeneous nuclear ribonucleoprotein K
<222>  (1)..(463)
<223>  Accession No. as of 09 Dec 2002: Q07244
<400>  28

Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn
1               5                   10                  15

Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala
            20                  25                  30

Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu
        35                  40                  45

Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn
            50                  55                  60

Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp
65                  70                  75                  80

Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr
            85                  90                  95

Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu
            100                 105                 110

Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp
```

```
            115                 120                 125

Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp
            130                 135                 140

Cys Glu Leu Arg Leu His Gln Ser Leu Ala Gly Gly Ile Ile
145                 150                 155                 160

Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr
            165                 170                 175

Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val
            180                 185                 190

Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile
            195                 200                 205

Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro
            210                 215                 220

Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr
225                 230                 235                 240

Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg
            245                 250                 255

Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro
            260                 265                 270

Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly
            275                 280                 285

Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala
            290                 295                 300

Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu
```

```
305             310             315             320
Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met
                325             330             335
    Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp
5               340             345             350
    Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly
    355             360             365
    Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly
                370             375             380
10  Gly Pro Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly
                385             390             395             400
    Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu
                405             410             415
15  Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp
                420             425             430
    Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln
                435             440             445
    Tyr Leu Leu Gln Asn Ser Val Lys Gln Tyr Ser Gly Lys Phe Phe
                450             455             460
20
```

<210> 29
<211> 172
<212> PRT

<213> Homo sapiens

<220>

<221> Translationally controlled tumor protein (TCTP)

<222> (1)..(172)

<223> Accession No. as of 09 Dec 2002: P13693

<400> 29

```
Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp
1               5               10              15
Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu
                20              25              30
Gly Lys Met Val Ser Arg Thr Gly Asn Ile Asp Asp Ser Leu Ile
35              40              45
Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
15  50              55              60
Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
65              70              75              80
Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
                85              90              95
Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
20              100             105             110
Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
                115             120             125
Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
```

```
                    130               135               140
Met Val Ala Leu Asp Leu Tyr Arg Glu Asp Gly Val Thr Pro Tyr Met

                    145               150           155           160
Ile Phe Phe Asp Gly Leu Glu Met Glu Lys Cys

  5                 165               170
```

```
<210>  30
<211>  284
<212>  PRT
 10
<213>  Homo sapiens
<220>
<221>  Tropomyosin 1 alpha chain
<222>  (1)..(284)
<223>  Accession No. as of 06 Dec 2002: P09493
 15
<400>  30

Met Asp Ala Ile Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu
  1                 5                 10                15

Asn Ala Leu Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys Ala Ala
                    20                25                30
 20
Glu Asp Arg Ser Lys Gln Leu Glu Asp Glu Leu Val Ser Leu Gln Lys
                    35                40                45

Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr Ser Glu Ala Leu
```

```
Lys Asp Ala Gln Glu Lys Leu Glu Leu Ala Glu Lys Lys Ala Thr Asp
                    50                55                60

Glu Glu Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu
                    65                70                75            80

Ala Glu Ala Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu
  5                 85                90                95

Glu Glu Leu Asp Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys
                    100               105               110

Leu Glu Glu Ala Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys
                    115               120               125

 10 Val Ile Glu Ser Arg Ala Gln Lys Asp Glu Glu Lys Met Glu Ile Gln
                    130               135               140

Glu Ile Gln Leu Lys Glu Ala Lys His Ile Ala Glu Asp Ala Asp Arg
                    145               150           155           160

Lys Tyr Glu Glu Val Ala Arg Lys Leu Val Ile Ile Glu Ser Asp Leu
 15                 165               170               175

Glu Arg Ala Glu Glu Arg Ala Glu Leu Ser Glu Gly Lys Cys Ala Glu
                    180               185               190

Leu Glu Glu Leu Lys Thr Val Thr Asn Asn Leu Lys Ser Leu Glu
                    195               200               205

 20 Ala Gln Ala Glu Lys Tyr Ser Gln Lys Glu Asp Arg Tyr Glu Glu Glu
                    210               215               220

Ile Lys Val Leu Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu
                    225               230               235           240

Phe Ala Glu Arg Ser Val Thr Lys Leu Glu Lys Ser Ile Asp Asp Leu
```

```
                                      50                  55                  60
Ser Ala Gln Gly Ala Gln Ile Gly Ala Met Leu Met Ala Ile Arg Leu
       65                  70                  75                  80

Arg Gly Met Asp Leu Glu Glu Thr Ser Val Leu Thr Gln Ala Leu Ala
       85                  90                  95
5
Gln Ser Gly Gln Leu Glu Trp Pro Glu Ala Trp Arg Gln Gln Leu
              100                 105                 110

Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Lys Val Ser Leu Val
              115                 120                 125

10  Leu Ala Pro Ala Leu Ala Ala Cys Gly Cys Lys Val Pro Met Ile Ser
              130                 135                 140

Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu Ser
       145                 150                 155                 160

Ile Pro Gly Phe Asn Val Ile Gln Ser Pro Glu Gln Met Gln Val Leu
              165                 170                 175

15  Leu Asp Gln Ala Gly Cys Cys Ile Val Gly Gln Ser Glu Gln Leu Val
              180                 185                 190

Pro Ala Asp Gly Ile Leu Tyr Ala Ala Arg Asp Val Thr Ala Thr Val
              195                 200                 205

20  Asp Ser Leu Pro Leu Ile Thr Ala Ser Ile Leu Ser Lys Lys Leu Val
              210                 215                 220

Glu Gly Leu Ser Ala Leu Val Val Asp Val Lys Phe Gly Gly Ala Ala
              225                 230                 235                 240

Val Phe Pro Asn Gln Glu Gln Ala Arg Glu Leu Ala Lys Thr Leu Val
```

```
              245                 250                 255
Glu Asp Glu Leu Tyr Ala Gln Lys Leu Lys Tyr Lys Ala Ile Ser Glu
              260                 265                 270

Glu Leu Asp His Ala Leu Asn Asp Met Thr Ser Ile
5             275                 280


    <210>   31
    <211>   482
10  <212>   PRT
    <213>   Homo sapiens
    <220>
    <221>   Thymidine phosphorylase precursor
    <222>   (1)..(482)
15  <223>   Accession No. as of 09 Dec 2002: P19971
    <400>   31

Met Ala Ala Leu Met Thr Pro Gly Thr Gly Ala Pro Pro Ala Pro Gly
1             5                   10                  15

Asp Phe Ser Gly Glu Gly Ser Gln Gly Leu Pro Asp Pro Ser Pro Glu
20  20            25                  30

Pro Lys Gln Leu Pro Glu Ile Leu Arg Met Lys Arg Asp Gly Gly Arg
       35                  40                  45

Leu Ser Glu Ala Asp Ile Arg Gly Phe Val Ala Ala Val Val Asn Gly
```

Gly Val Gly Ala Ser Leu Gly Arg Val Ala Ala Leu Thr Ala
  245   250   255

Met Lys Pro Leu Gly Arg Cys Val Gly His Ala Leu Glu Val Glu
  260   265   270

5

Glu Ala Leu Leu Cys Met Asp Gly Ala Gly Pro Asp Leu Arg Asp
  275   280   285

  290   295   300

Leu Val Thr Thr Leu Gly Gly Ala Leu Leu Trp Leu Ser Gly His Ala
  305   310   315   320

10 Gly Thr Gln Ala Gln Ala Ala Arg Val Ala Ala Ala Ala Leu Asp Asp
  325   330   335

Gly Ser Ala Leu Gly Arg Phe Glu Arg Met Leu Ala Ala Gln Gly Val
  340   345   350

Asp Pro Gly Leu Ala Arg Ala Leu Cys Ser Gly Ser Pro Ala Glu Arg
  355   360   365

15 Arg Gln Leu Leu Pro Arg Ala Arg Glu Gln Glu Glu Leu Ala Pro
  370   375   380

Ala Asp Gly Thr Val Glu Leu Val Arg Ala Leu Pro Leu Ala Leu Val
  385   390   395   400

20 Leu His Glu Leu Gly Ala Gly Arg Ser Arg Ala Gly Glu Pro Leu Arg
  405   410   415

Leu Gly Val Gly Ala Glu Leu Leu Val Asp Val Gly Gln Arg Leu Arg
  420   425   430

Arg Gly Thr Pro Trp Leu Arg Val His Arg Asp Gly Pro Ala Leu Ser

Gly Pro Gln Ser Arg Ala Leu Gln Glu Ala Leu Val Leu Ser Asp Arg
  435   440   445

Ala Pro Phe Ala Ala Pro Leu Pro Phe Ala Glu Gly Leu Val Leu Pro Pro
  450   455   460

5   465   470   475   480

Gln Gln

10 <210> 32

<211> 488

<212> PRT

<213> Homo sapiens

<220>

15 <221> Cytosol aminopeptidase

<222> (1)..(488)

<223> Accession No. as of 09 Dec 2002: P28838

<400> 32

20 Met Thr Lys Gly Leu Val Leu Gly Ile Tyr Ser Lys Glu Lys Glu Asp
  1   5   10   15

Asp Val Pro Gln Phe Thr Ser Ala Gly Glu Asn Phe Asp Lys Leu Leu
  20   25   30

Ala Gly Lys Leu Arg Glu Thr Leu Asn Ile Ser Gly Pro Pro Leu Lys

                    35
Ala Gly Lys Thr Arg Thr Phe Tyr Gly Leu His Gln Asp Phe Pro Ser
              40   45
        50   55   60
Val Val Leu Val Gly Leu Gly Lys Lys Ala Ala Gly Ile Asp Glu Gln
5   65   70   75   80
Glu Asn Trp His Glu Gly Lys Glu Asn Ile Arg Ala Ala Val Ala Ala
              85   90   95
Gly Cys Arg Gln Ile Gln Asp Leu Glu Ser Ser Val Glu Val Asp
              100   105   110
10 Pro Cys Asp Asp Gln Ala Ala Ala Glu Ala Gly Ala Val Leu Gly Leu
        115   120   125
Tyr Glu Tyr Asp Leu Lys Gln Lys Lys Lys Met Ala Val Ser Ala
        130   135   140
Lys Leu Tyr Gly Ser Gly Asp Gln Glu Ala Trp Gln Lys Gly Val Leu
15 145   150   155   160
Phe Ala Ser Gly Gln Asn Leu Ala Arg Gln Leu Met Glu Thr Pro Ala
        165   170   175
Asn Glu Met Thr Pro Thr Arg Phe Ala Glu Ile Ile Glu Lys Asn Leu
        180   185   190
20 Lys Ser Ala Ser Ser Lys Thr Glu Val His Ile Arg Pro Lys Ser Trp
        195   200   205
Ile Glu Gln Ala Met Gly Ser Phe Leu Ser Val Ala Lys Gly Ser
        210   215   220
Asp Glu Pro Pro Val Phe Leu Glu Ile His Tyr Lys Gly Ser Pro Asn

        225   230   235   240
Ala Asn Glu Pro Leu Val Phe Val Gly Lys Gly Ile Phe Asp
                    245   250   255
Ser Gly Gly Ile Ser Ile Lys Ala Ser Ala Asn Met Asp Leu Met Arg
5   260   265   270
Ala Asp Met Gly Gly Ala Ala Thr Ile Cys Ser Ala Ile Val Ser Ala
        275   280   285
Ala Lys Leu Asn Leu Pro Ile Asn Ile Ile Gly Leu Ala Pro Leu Cys
        290   295   300
10 Glu Asn Met Pro Ser Gly Lys Ala Asn Lys Pro Gly Asp Val Val Arg
        305   310   315   320
Ala Lys Asn Gly Lys Thr Ile Gln Val Asp Asn Thr Asp Ala Glu Gly
                    325   330   335
Arg Leu Ile Leu Ala Asp Ala Leu Cys Tyr Ala His Thr Phe Asn Pro
15   340   345   350
Lys Val Ile Leu Asn Ala Ala Thr Leu Thr Gly Ala Met Asp Val Ala
        355   360   365
Leu Gly Ser Gly Ala Thr Gly Val Phe Thr Asn Ser Ser Trp Leu Trp
        370   375   380
20 Asn Lys Leu Phe Glu Ala Ser Ile Glu Thr Gly Asp Arg Val Trp Arg
        385   390   395   400
Met Pro Leu Phe Glu His Tyr Thr Arg Gln Val Val Asp Cys Gln Leu
        405   410   415
Ala Asp Val Asn Asn Ile Gly Lys Tyr Arg Ser Ala Gly Ala Cys Thr

```
                              420              425              430
Ala Ala Ala Phe Leu Lys Glu Phe Val Thr His Pro Lys Trp Ala His

                       435              440              445
Leu Asp Ile Ala Gly Val Met Thr Asn Lys Asp Glu Val Pro Tyr Leu

 5                     450              455              460
Arg Gly Met Thr Gly Arg Pro Thr Arg Thr Leu Ile Glu Phe Leu

                465              470              475              480
Leu Arg Phe Ser Gln Asp Asn Ala

                485
```

<210> 33
<211> 400
<212> PRT
<213> Homo sapiens
<220>
<221> Keratin, type I cytoskeletal 19
<222> (1)..(400)
<223> Accession No. as of 09 Dec 2002 : P08727

<400> 33

```
Met Thr Ser Tyr Ser Tyr Arg Gln Ser Ser Ala Thr Ser Ser Phe Gly
 1               5                    10                   15
```

```
Gly Leu Gly Gly Ser Val Arg Phe Gly Val Ala Phe Arg
                     20              25              30

Ala Pro Ser Ile His Gly Gly Ser Gly Gly Arg Gly Val Ser Val Ser
              35              40              45

 5 Ser Ala Arg Phe Val Ser Ser Ser Ser Gly Gly Tyr Gly Gly Gly
                 50              55              60

Tyr Gly Gly Val Leu Thr Ala Ser Asp Gly Leu Leu Ala Gly Asn Glu
 65              70              75              80

10 Lys Leu Thr Met Gln Asn Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp
                 85              90              95

Lys Val Arg Ala Leu Glu Ala Ala Asn Gly Glu Leu Glu Val Lys Ile
                 100             105             110

Arg Asp Trp Tyr Gln Lys Gln Gly Pro Gly Pro Ser Arg Asp Tyr Ser
              115             120             125

15 His Tyr Tyr Thr Thr Ile Gln Asp Leu Arg Asp Lys Ile Leu Gly Ala
                 130             135             140

Thr Ile Glu Asn Ser Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu
              145             150             155             160

Ala Ala Asp Asp Phe Arg Thr Lys Phe Glu Thr Glu Gln Ala Leu Arg
20              165             170             175

Met Ser Val Glu Ala Asp Ile Asn Gly Leu Arg Arg Val Leu Asp Glu
                 180             185             190

Leu Thr Leu Ala Arg Thr Asp Leu Glu Met Gln Ile Glu Gly Leu Lys
              195             200             205
```

```
       Glu Glu Leu Ala Tyr Tyr Leu Lys Lys Asn His Glu Glu Ile Ser Thr
       210             215                 220

       Leu Arg Gly Gln Val Gly Gly Gln Val Ser Val Asp Ser Ala
       225             230                 235                 240

  5    Pro Gly Thr Asp Leu Ala Lys Ile Leu Ser Asp Met Arg Ser Gln Tyr
       245                 250                 255

       Glu Val Met Ala Glu Gln Asn Arg Lys Asp Ala Glu Ala Trp Phe Thr
       260                 265                 270

       Ser Arg Thr Glu Leu Asn Arg Glu Val Ala Gly His Thr Glu Gln
  10   275                 280                 285

       Leu Gln Met Ser Arg Ser Glu Val Thr Asp Leu Arg Arg Thr Leu Gln
       290                 295                 300

       Gly Leu Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala Ala Leu
       305             310                 315                 320

  15   Glu Asp Thr Leu Ala Glu Thr Glu Ala Arg Phe Gly Ala Gln Leu Ala
       325                 330                 335

       His Ile Gln Ala Leu Ile Ser Gly Ile Glu Ala Gln Leu Ala Asp Val
       340                 345                 350

       Arg Ala Asp Ser Glu Arg Gln Asn Gln Glu Tyr Gln Arg Leu Met Asp
  20   355                 360                 365

       Ile Lys Ser Arg Leu Glu Gln Glu Ile Ala Thr Tyr Arg Ser Leu Leu
       370                 375                 380

       Glu Gly Gln Glu Asp His Tyr Asn Asn Leu Ser Ala Ser Lys Val Leu
       385             390                 395                 400
```

```
       <210>  34
       <211>  325
       <212>  PRT
  5    <213>  Homo sapiens

       <220>

       <221>  Alcohol dehydrogenase [NADP+]

       <222>  (1)..(325)

  10   <223>  Accession No. as of 09 Dec 2002: P14550

       <400>  34

       Met Ala Ala Ser Cys Val Leu Leu His Thr Gly Gln Lys Met Pro Leu
  1                 5                   10                  15

  15   Ile Gly Leu Gly Thr Trp Lys Ser Glu Pro Gly Gln Val Lys Ala Ala
       20                  25                  30

       Val Lys Tyr Ala Leu Ser Val Gly Tyr Arg His Ile Asp Cys Ala Ala
       35                  40                  45

       Ile Tyr Gly Asn Glu Pro Glu Ile Gly Glu Ala Leu Lys Glu Asp Val
  20   50                  55                  60

       Gly Pro Gly Lys Ala Val Pro Arg Glu Glu Leu Phe Val Thr Ser Lys
       65                  70                  75                  80

       Leu Trp Asn Thr Lys His His Pro Glu Asp Val Glu Pro Ala Leu Arg
       85                  90                  95
```

Lys Thr Leu Ala Asp Leu Gln Leu Glu Tyr Leu Asp Leu Tyr Leu Met
                  100   105   110

His Trp Pro Tyr Ala Phe Glu Arg Gly Asp Asn Pro Phe Pro Lys Asn
          115   120   125

5 Ala Asp Gly Thr Ile Cys Tyr Asp Ser Thr His Tyr Lys Glu Thr Trp
          130   135   140

Lys Ala Leu Glu Ala Leu Val Ala Lys Gly Leu Val Gln Ala Leu Gly
          145   150   155   160

Leu Ser Asn Phe Asn Ser Arg Gln Ile Asp Asp Ile Leu Ser Val Ala
10   165   170   175

Ser Val Arg Pro Ala Val Leu Gln Val Glu Cys His Pro Tyr Leu Ala
          180   185   190

Gln Asn Glu Ile Leu Ala His Cys Gln Ala Arg Gly Leu Glu Val Thr
          195   200   205

15 Ala Tyr Ser Pro Leu Gly Ser Ser Asp Arg Ala Trp Arg Asp Pro Asp
          210   215   220

Glu Pro Val Leu Leu Glu Glu Pro Val Val Leu Ala Leu Ala Glu Lys
          225   230   235   240

Tyr Gly Arg Ser Pro Ala Gln Ile Leu Leu Arg Trp Gln Val Gln Arg
20   245   250   255

Lys Val Ile Cys Ile Pro Lys Ser Ile Thr Pro Ser Arg Ile Leu Gln
          260   265   270

Asn Ile Lys Val Phe Asp Phe Thr Phe Ser Pro Glu Glu Met Lys Gln
          275   280   285

Leu Asn Ala Leu Asn Lys Asn Trp Arg Tyr Ile Val Pro Met Leu Thr
          290   295   300

Val Asp Gly Lys Arg Val Pro Arg Asp Ala Gly His Pro Leu Tyr Pro
          305   310   315   320

5 Phe Asn Asp Pro Tyr
          325

<210> 35
10 <211> 270
<212> PRT
<213> Homo sapiens
<220>
<221> Elastase IIIA precursor
15 <222> (1)..(270)
<223> Accession No. as of 09 Dec 2002: P09093
<400> 35

Met Met Leu Arg Leu Leu Ser Ser Leu Leu Leu Val Ala Val Ala Ser
20 1   5   10   15

Gly Tyr Gly Pro Ser Ser His Ser Ser Arg Val Val His Gly
          20   25   30

Glu Asp Ala Val Pro Tyr Ser Trp Pro Trp Gln Val Ser Leu Gln Tyr
          35   40   45

Glu Lys Gly Ser Phe Tyr His Thr Cys Gly Gly Ser Leu Ile Ala
50   55   60

Pro Asp Trp Val Val Thr Ala Gly His Cys Ile Ser Arg Asp Leu Thr
65   70   75   80

Tyr Gln Val Val Leu Gly Glu Tyr Asn Leu Ala Val Lys Glu Gly Pro
85   90   95

Glu Gln Val Ile Pro Ile Asn Ser Glu Glu Leu Phe Val His Pro Leu
100   105   110

Trp Asn Arg Ser Cys Val Ala Cys Gly Asn Asp Ile Ala Leu Ile Lys
115   120   125

Leu Ser Arg Ser Ala Gln Leu Gly Asp Ala Val Gln Leu Ala Ser Leu
130   135   140

Pro Pro Ala Gly Asp Ile Leu Pro Asn Lys Thr Pro Cys Tyr Ile Thr
145   150   155   160

Gly Trp Gly Arg Leu Tyr Thr Asn Gly Pro Leu Pro Asp Lys Leu Gln
165   170   175

Gln Ala Arg Leu Pro Val Val Asp Tyr Lys His Cys Ser Arg Trp Asn
180   185   190

Trp Trp Gly Ser Thr Val Lys Lys Thr Met Val Cys Ala Gly Gly Tyr
195   200   205

Ile Arg Ser Gly Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Pro
210   215   220

Thr Glu Asp Gly Gly Trp Gln Val His Gly Val Thr Ser Phe Val Ser
225   230   235   240

Gly Phe Gly Cys Asn Phe Ile Trp Lys Pro Thr Val Phe Thr Arg Val
245   250   255

Ser Ala Phe Ile Asp Trp Ile Glu Glu Thr Ile Ala Ser His
260   265   270

5

<210> 36
<211> 509
<212> PRT
10 <213> Homo sapiens
<220>
<221> Dihydrolipoamide dehydrogenase, mitochondrial precursor
<222> (1)..(509)
<223> Accession No. as of 09 Dec 2002: P09622
15 <400> 36

Met Gln Ser Trp Ser Arg Val Tyr Cys Ser Leu Ala Lys Arg Gly His
1   5   10   15

Phe Asn Arg Ile Ser His Gly Leu Gln Gly Leu Ser Ala Val Pro Leu
20   25   30

Arg Thr Tyr Ala Asp Gln Pro Ile Asp Ala Asp Val Thr Val Ile Gly
35   40   45

Ser Gly Pro Gly Gly Tyr Val Ala Ala Ile Lys Ala Ala Gln Leu Gly
50   55   60

Phe Lys Thr Val Cys Ile Glu Lys Asn Glu Thr Leu Gly Gly Thr Cys
65   70   75   80

Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Leu Asn Asn Ser His
                85   90   95

Tyr Tyr His Met Ala His Gly Thr Asp Phe Ala Ser Arg Gly Ile Glu
5   100   105   110

Met Ser Glu Val Arg Leu Asn Asp Lys Met Met Glu Gln Lys Ser
                115   120   125

Thr Ala Val Lys Ala Leu Thr Gly Gly Ile Ala His Leu Phe Lys Gln
10   130   135   140

Asn Lys Val Val His Val Asn Gly Tyr Gly Lys Ile Thr Gly Lys Asn
        145   150   155   160

Gln Val Thr Ala Thr Lys Ala Asp Gly Gly Gln Val Ile Asp Thr
                165   170   175

Lys Asn Ile Leu Ile Ala Thr Gly Ser Glu Val Thr Pro Phe Pro Gly
15   180   185   190

Ile Thr Ile Asp Glu Asp Thr Ile Val Ser Ser Thr Gly Ala Leu Ser
                195   200   205

Leu Lys Lys Val Pro Glu Lys Met Val Val Ile Gly Ala Gly Val Ile
                210   215   220

Gly Val Glu Leu Gly Ser Val Trp Gln Arg Leu Gly Ala Asp Val Thr
20   225   230   235   240

Ala Val Glu Phe Leu Gly His Val Gly Gly Val Gly Ile Asp Met Glu
                245   250   255

Ile Ser Lys Asn Phe Gln Arg Ile Leu Gln Lys Gln Gly Phe Lys Phe
                260   265   270

Lys Leu Asn Thr Lys Val Thr Gly Ala Thr Lys Ser Asp Gly Lys
                275   280   285

Ile Asp Val Ser Ile Glu Ala Ala Ser Gly Gly Lys Ala Glu Val Ile
5   290   295   300

Thr Cys Asp Val Leu Leu Val Cys Ile Gly Arg Arg Pro Phe Thr Lys
                305   310   315   320

Asn Leu Gly Leu Glu Glu Leu Gly Ile Glu Leu Asp Pro Arg Gly Arg
                325   330   335

Ile Pro Val Asn Thr Arg Phe Gln Thr Lys Ile Pro Asn Ile Tyr Ala
10   340   345   350

Ile Gly Asp Val Val Ala Gly Pro Met Leu Ala His Lys Ala Glu Asp
                355   360   365

Glu Gly Ile Ile Cys Val Glu Gly Met Ala Gly Ala Gly Ala Val His Ile
15   370   375   380

Asp Tyr Asn Cys Val Pro Ser Val Ile Tyr Thr His Pro Glu Val Ala
                385   390   395   400

Trp Val Gly Lys Ser Glu Gln Leu Lys Glu Gly Ile Glu Tyr
                405   410   415

Lys Val Gly Lys Phe Pro Phe Ala Ala Asn Ser Arg Ala Lys Thr Asn
20   420   425   430

Ala Asp Thr Asp Gly Met Val Lys Ile Leu Gly Gln Lys Ser Thr Asp
                435   440   445

Phe Glu Tyr Ile Ile Ala Glu Lys Arg Gly Lys Asn Asn Thr Val Gly
                   35   40   45

Leu Ile Gln Leu Asn Arg Pro Lys Ala Leu Asn Ala Leu Cys Asp Gly
      50   55   60

5 Leu Ile Asp Glu Leu Asn Gln Ala Leu Lys Ile Phe Glu Glu Asp Pro
      65   70   75   80

Ala Val Gly Ala Ile Val Leu Thr Gly Gly Lys Ala Phe Ala Ala
              85   90   95

Gly Ala Asp Ile Lys Glu Met Gln Asn Leu Ser Phe Gln Asp Cys Tyr
10   100   105   110

Ser Ser Lys Phe Leu Lys His Asp His Leu Thr Gln Val Lys Lys
            115   120   125

Pro Val Ile Ala Ala Val Asn Gly Tyr Ala Phe Gly Gly Gly Cys Glu
    130   135   140

15 Leu Ala Met Met Cys Asp Ile Ile Tyr Ala Gly Glu Lys Ala Gln Phe
      145   150   155   160

Ala Gln Pro Glu Ile Leu Ile Gly Thr Ile Pro Gly Ala Gly Gly Thr
    165   170   175

Gln Arg Leu Thr Arg Ala Val Gly Lys Ser Leu Ala Met Glu Met Val
20   180   185   190

Leu Thr Gly Asp Arg Ile Ser Ala Gln Asp Ala Lys Gln Ala Gly Leu
    195   200   205

Val Ser Lys Ile Cys Pro Val Glu Thr Leu Val Glu Glu Ala Ile Gln
    210   215   220

Arg Val Leu Gly Ala His Ile Leu Leu Gly Pro Gly Ala Gly Glu Met Val
    450   455   460

Asn Glu Ala Ala Leu Ala Leu Glu Tyr Gly Ala Ser Cys Glu Asp Ile
    465   470   475   480

5 Ala Arg Val Cys His Ala His Pro Thr Leu Ser Glu Ala Phe Arg Glu
      485   490   495

Ala Asn Leu Ala Ala Ser Phe Gly Lys Ser Ile Asn Phe
        500   505

10

<210> 37
<211> 290
<212> PRT
<213> Homo sapiens
<220>
15 <221> Enoyl-CoA hydratase, mitochondrial precursor
<222> (1)..(290)
<223> Accession No. as of 09 Dec 2002: P30084
<400> 37

20

Met Ala Ala Leu Arg Val Leu Leu Ser Cys Ala Arg Gly Pro Leu Arg
1   5   10   15

Pro Pro Val Arg Cys Pro Ala Trp Arg Pro Phe Ala Ser Gly Ala Asn
      20   25   30

Ala Pro Leu Pro Gly Leu Ser Ala Pro Gly Arg Leu Phe Asp Gln Arg
                20   25   30

Phe Gly Glu Gly Leu Leu Glu Ala Glu Ala Ala Leu Cys Pro Thr
             35   40   45

5 Thr Leu Ala Pro Tyr Tyr Leu Arg Ala Pro Ser Val Ala Leu Pro Val
               50   55   60

Ala Gln Val Pro Thr Asp Pro Gly His Phe Ser Val Leu Leu Asp Val
  65   70   75   80

Lys His Phe Ser Pro Glu Glu Ile Ala Val Lys Val Val Gly Glu His
10   85   90   95

Val Glu Val His Ala Arg His Glu Glu Arg Pro Asp Glu His Gly Phe
             100   105   110

Val Ala Arg Glu Phe His Arg Arg Tyr Arg Leu Pro Pro Gly Val Asp
             115   120   125

15 Pro Ala Ala Val Thr Ser Ala Leu Ser Pro Glu Gly Val Leu Ser Ile
             130   135   140

Gln Ala Ala Pro Ala Ser Ala Gln Ala Pro Pro Ala Ala Ala Lys
  145   150   155   160

20

<210> 39
<211> 151
<212> PRT
<213> Homo sapiens

Cys Ala Glu Lys Ile Ala Ser Asn Ser Lys Ile Val Val Ala Met Ala
  225   230   235   240

Lys Glu Ser Val Asn Ala Ala Phe Glu Met Thr Leu Thr Glu Gly Ser
             245   250   255

5 Lys Leu Glu Lys Lys Leu Phe Tyr Ser Thr Phe Ala Thr Asp Asp Arg
             260   265   270

Lys Glu Gly Met Thr Ala Phe Val Glu Lys Lys Arg Lys Ala Asn Phe Lys
             275   280   285

Asp Gln
10 290

<210> 38
<211> 160
<212> PRT
<213> Homo sapiens
<220>
<221> Heat-shock 20 kDa like-protein p20
<222> (1)..(160)
20 <223> Accession No. as of 09 Dec 2002: O14558

<400> 38

Met Glu Ile Pro Val Pro Val Gln Pro Ser Trp Leu Arg Arg Ala Ser
1   5   10   15

<220>

<221> Myosin light chain alkali, non-muscle isoform

<222> (1)..(151)

<223> Accession No. as of 09 Dec 2002: P16475

<400> 39

```
Met Cys Asp Phe Thr Glu Asp Gln Thr Ala Glu Phe Lys Glu Ala Phe
1                   5                   10                  15
Gln Leu Phe Asp Arg Thr Gly Asp Gly Lys Ile Leu Tyr Ser Gln Cys
            20                  25                  30
Gly Asp Val Met Arg Ala Leu Gly Gln Asn Pro Thr Asn Ala Glu Val
        35                  40                  45
Leu Lys Val Leu Gly Asn Pro Lys Ser Asp Glu Met Asn Val Lys Val
    50                  55                  60
Leu Asp Phe Glu His Phe Leu Pro Met Leu Gln Thr Val Ala Lys Asn
65                  70                  75                  80
Lys Asp Gln Gly Thr Tyr Glu Asp Tyr Val Glu Gly Leu Arg Val Phe
            85                  90                  95
Asp Lys Glu Gly Asn Gly Thr Val Met Gly Ala Glu Ile Arg His Val
            100                 105                 110
Leu Val Thr Leu Gly Glu Lys Met Thr Glu Glu Val Glu Met Leu
        115                 120                 125
Val Ala Gly His Glu Asp Ser Asn Gly Cys Ile Asn Tyr Glu Ala Phe
    130                 135                 140
```

```
Val Arg His Ile Leu Ser Gly
145                 150
```

<210> 40

<211> 592

<212> PRT

<213> Homo sapiens

<220>

<221> Calnexin precursor

<222> (1)..(592)

<223> Accession No. as of 09 Dec 2002: P27824

<400> 40

```
Met Glu Gly Lys Trp Leu Leu Cys Met Leu Leu Val Leu Gly Thr Ala
1                   5                   10                  15
Ile Val Glu Ala His Asp Gly His Asp Asp Asp Val Ile Asp Ile Glu
            20                  25                  30
Asp Asp Leu Asp Asp Val Ile Glu Glu Val Glu Asp Ser Lys Pro Asp
        35                  40                  45
Thr Thr Ala Pro Pro Ser Ser Pro Lys Val Thr Tyr Lys Ala Pro Val
        50                  55                  60
Pro Thr Gly Glu Val Tyr Phe Ala Asp Ser Phe Asp Arg Gly Thr Leu
65                  70                  75                  80
```

Ser Gly Trp Ile Leu Ser Lys Ala Lys Asp Asp Thr Asp Asp Glu
     85   90   95

Ile Ala Lys Tyr Asp Gly Lys Trp Glu Val Glu Glu Met Lys Glu Ser
     100   105   110

Lys Leu Pro Gly Asp Lys Gly Leu Val Leu Met Ser Arg Ala Lys His
5   115   120   125

His Ala Ile Ser Ala Lys Leu Asn Lys Pro Phe Leu Phe Asp Thr Lys
     130   135   140

Pro Leu Ile Val Gln Tyr Glu Val Asn Phe Gln Asn Gly Ile Glu Cys
10   145   150   155   160

Gly Gly Ala Tyr Val Lys Leu Leu Ser Lys Thr Pro Glu Leu Asn Leu
     165   170   175

Asp Gln Phe His Asp Lys Pro Tyr Thr Ile Met Phe Gly Pro Asp
     180   185   190

Lys Cys Gly Glu Asp Tyr Lys Leu His Phe Ile Phe Arg His Lys Asn
15   195   200   205

Pro Lys Thr Gly Ile Tyr Glu Lys His Ala Lys Arg Pro Asp Ala
     210   215   220

Asp Leu Lys Thr Tyr Phe Thr Asp Lys Lys Thr His Leu Tyr Thr Leu
20 225   230   235   240

Ile Leu Asn Pro Asp Asn Ser Phe Glu Ile Leu Val Asp Gln Ser Val
     245   250   255

Val Asn Ser Gly Asn Leu Leu Asn Asp Met Thr Pro Pro Val Asn Pro
     260   265   270

Ser Arg Glu Ile Glu Asp Pro Glu Asp Arg Lys Pro Glu Asp Trp Asp
     275   280   285

Glu Arg Pro Lys Ile Pro Asp Pro Glu Ala Val Lys Pro Asp Asp Trp
     290   295   300

Asp Glu Asp Ala Pro Ala Lys Ile Pro Asp Glu Glu Ala Thr Lys Pro
5   305   310   315   320

Glu Gly Trp Leu Asp Asp Glu Pro Glu Tyr Val Pro Asp Pro Asp Ala
     325   330   335

Glu Lys Pro Glu Asp Trp Asp Glu Asp Met Asp Gly Glu Trp Glu Ala
10   340   345   350

Pro Gln Ile Ala Asn Pro Arg Cys Glu Ser Ala Pro Gly Cys Gly Val
     355   360   365

Trp Gln Arg Pro Val Ile Asp Asn Pro Asn Tyr Lys Gly Lys Trp Lys
     370   375   380

Pro Pro Met Ile Asp Asn Pro Ser Tyr Gln Gly Ile Trp Lys Pro Arg
15   385   390   395   400

Lys Ile Pro Asn Pro Asp Phe Phe Glu Asp Leu Glu Pro Phe Arg Met
     405   410   415

Thr Pro Phe Ser Ala Ile Gly Leu Glu Leu Trp Ser Met Thr Ser Asp
20   420   425   430

Ile Phe Phe Asp Asn Phe Ile Ile Cys Ala Asp Arg Arg Ile Val Asp
     435   440   445

Asp Trp Ala Asn Asp Gly Trp Gly Leu Lys Lys Ala Ala Asp Gly Ala
     450   455   460

```
Ala Glu Pro Gly Val Val Gly Gln Met Ile Glu Ala Ala Glu Glu Arg
465                 470                 475             480

Pro Trp Leu Trp Val Val Tyr Ile Leu Thr Val Ala Leu Pro Val Phe
                485                 490                 495

Leu Val Ile Leu Phe Cys Cys Ser Gly Lys Gln Thr Ser Gly Met
5               500                 505                 510

Glu Tyr Lys Lys Thr Asp Ala Pro Gln Pro Asp Val Lys Glu Glu Glu
                515                 520                 525

Glu Glu Lys Glu Glu Glu Lys Asp Lys Gly Asp Glu Glu Glu Glu Gly
10              530                 535                 540

Glu Glu Lys Leu Glu Glu Lys Gln Lys Ser Asp Ala Glu Glu Asp Gly
                545                 550                 555             560

Gly Thr Val Ser Gln Glu Glu Glu Asp Arg Lys Pro Lys Ala Glu Glu
                565                 570                 575

Asp Glu Ile Leu Asn Arg Ser Pro Asn Arg Lys Pro Arg Arg Glu
15              580                 585                 590
```

```
<210> 41
<211> 282
<212> PRT
<213> Homo sapiens
<220>
<221> Complement component 1
```

```
<222> (1)..(282)
<223> Accession No. as of 09 Dec 2002: Q07021

<400> 41

Met Leu Pro Leu Leu Arg Cys Val Pro Arg Val Leu Gly Ser Ser Val
5   1               5                   10                  15

Ala Gly Leu Arg Ala Ala Ala Pro Ala Ser Pro Phe Arg Gln Leu Leu
                20                  25                  30

Gln Pro Ala Pro Arg Leu Cys Thr Arg Pro Phe Gly Leu Leu Ser Val
10          35                  40                  45

Arg Ala Gly Ser Glu Arg Arg Gly Leu Leu Arg Pro Arg Gly Pro
            50                  55                  60

Cys Ala Cys Gly Cys Gly Cys Gly Ser Leu His Thr Asp Gly Asp Lys
            65                  70                  75              80

Ala Phe Val Asp Leu Ser Asp Glu Ile Lys Glu Glu Arg Lys Ile
15          85                  90                  95

Gln Lys His Lys Thr Leu Pro Lys Met Ser Gly Gly Trp Glu Leu Glu
                100                 105                 110

Leu Asn Gly Thr Glu Ala Lys Leu Val Arg Lys Val Ala Gly Glu Lys
20          115                 120                 125

Ile Thr Val Thr Phe Asn Ile Asn Ser Ile Pro Pro Thr Phe Asp
                130                 135                 140

Gly Glu Glu Pro Ser Gln Gly Gln Lys Val Glu Glu Gln Glu Pro
145                 150                 155                 160
```

Glu Leu Ser Thr Pro Asn Phe Val Glu Val Ile Lys Asn Asp
                165   170   175

Asp Gly Lys Lys Ala Leu Val Leu Asp Cys His Tyr Pro Glu Asp Glu
            180   185   190

5   Val Gly Gln Glu Asp Glu Ala Gly Ile Phe Ser Ile Arg Glu
                195   200   205

Val Ser Phe Gln Ser Thr Gly Glu Ser Glu Trp Lys Asp Thr Asn Tyr
            210   215   220

Thr Leu Asn Thr Asp Ser Leu Asp Trp Ala Leu Tyr Asp His Leu Met
10 225   230   235   240

Asp Phe Leu Ala Asp Arg Gly Val Asp Asn Thr Phe Ala Asp Glu Leu
            245   250   255

Val Glu Leu Ser Thr Ala Leu Glu His Gln Glu Tyr Ile Thr Phe Leu
            260   265   270

15 Glu Asp Leu Lys Ser Phe Val Lys Ser Gln
                275   280

<210> 42
20 <211> 727
<212> PRT
<213> Homo sapiens
<220>
<221> NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

precursor

<222> (1)..(727)
<223> Accession No. as of 09 Dec 2002: P28331
<400> 42

5

Met Leu Arg Ile Pro Val Arg Arg Ala Leu Val Gly Leu Ser Lys Ser
1   5   10   15

Pro Lys Gly Cys Val Arg Thr Thr Ala Thr Ala Ala Ser Asn Leu Ile
                20   25   30

10 Glu Val Phe Val Asp Gly Gln Ser Val Met Val Glu Pro Gly Thr Thr
                35   40   45

Val Leu Gln Ala Cys Glu Lys Val Gly Met Gln Ile Pro Arg Phe Cys
50   55   60

Tyr His Glu Arg Leu Ser Val Ala Gly Asn Cys Arg Met Cys Leu Val
15 65   70   75   80

Glu Ile Glu Lys Ala Pro Lys Val Val Ala Ala Cys Ala Met Pro Val
                85   90   95

Met Lys Gly Trp Asn Ile Leu Thr Asn Ser Glu Lys Ser Lys Ala
                100   105   110

20 Arg Glu Gly Val Met Glu Phe Leu Leu Ala Asn His Pro Leu Asp Cys
                115   120   125

Pro Ile Cys Asp Gln Gly Gly Glu Cys Asp Leu Gln Asp Gln Ser Met
            130   135   140

Met Phe Gly Asn Asp Arg Ser Arg Phe Leu Glu Gly Lys Arg Ala Val

145   150   155   160

Glu Asp Lys Asn Ile Gly Pro Leu Val Lys Thr Ile Met Thr Arg Cys

     165   170   175

Ile Gln Cys Thr Arg Cys Ile Arg Phe Ala Ser Glu Ile Ala Gly Val

5   180   185   190

Asp Asp Leu Gly Thr Gly Arg Gly Asn Asp Met Gln Val Gly Thr

     195   200   205

Tyr Ile Glu Lys Met Phe Met Ser Glu Leu Ser Gly Asn Ile Ile Asp

     210   215   220

10 Ile Cys Pro Val Gly Ala Leu Thr Ser Lys Pro Tyr Ala Phe Thr Ala

     225   230   235   240

Arg Pro Trp Glu Thr Arg Lys Thr Glu Ser Ile Asp Val Met Asp Ala

     245   250   255

Val Gly Ser Asn Ile Val Val Ser Thr Arg Thr Gly Glu Val Met Arg

15   260   265   270

Ile Leu Pro Arg Met His Glu Asp Ile Asn Glu Glu Trp Ile Ser Asp

     275   280   285

Lys Thr Arg Phe Ala Tyr Asp Gly Leu Lys Arg Gln Arg Leu Thr Glu

20   290   295   300

Pro Met Val Arg Asn Glu Asn Lys Gly Gly Leu Leu Thr Tyr Thr Ser Trp Glu

     305   310   315   320

Asp Ala Leu Ser Arg Val Ala Gly Met Leu Gln Ser Phe Gln Gly Lys

     325   330   335

Asp Val Ala Ala Ile Ala Gly Gly Leu Val Asp Ala Glu Ala Leu Val

---

     340   345   350

Ala Leu Lys Asp Leu Leu Asn Arg Val Asp Ser Asp Thr Leu Cys Thr

     355   360   365

Glu Glu Val Phe Pro Thr Ala Gly Ala Gly Thr Ala Gly Leu Arg Ser Asn

5   370   375   380

Tyr Leu Asn Thr Thr Ile Ala Gly Val Glu Ala Asp Val Val

     385   390   395   400

Leu Leu Val Gly Thr Asn Pro Arg Phe Glu Ala Pro Leu Phe Asn Ala

     405   410   415

10 Trp Ile Arg Lys Ser Trp Leu His Asn Asp Leu Lys Val Ala Leu Ile

     420   425   430

Gly Ser Pro Val Asp Leu Thr Tyr Thr Tyr Asp His Leu Gly Asp Ser

     435   440   445

Pro Lys Ile Leu Gln Asp Ile Ala Ser Gly Ser His Pro Phe Ser Gln

15   450   455   460

Val Leu Lys Glu Ala Lys Lys Pro Met Val Val Leu Gly Ser Ser Ala

     465   470   475   480

Leu Gln Arg Asn Asp Gly Ala Ala Ile Leu Ala Ala Leu Asp Leu

     485   490   495

Ala Gln Lys Ile Arg Met Thr Ser Gly Val Gly Asp Trp Lys Val

20   500   505   510

Met Asn Ile Leu His Arg Ile Ala Ser Gln Val Ala Ala Leu Asp Leu

     515   520   525

Gly Tyr Lys Pro Gly Val Glu Ala Ile Arg Lys Asn Pro Pro Lys Val

725

<210> 43
<211> 491
<212> PRT
<213> Homo sapiens
<220>
<221> Pre-B cell enhancing factor precursor
<222> (1)..(491)
<223> Accession No. as of 09 Dec 2002: P43490
<400> 43

Met Asn Pro Ala Ala Glu Ala Glu Phe Asn Ile Leu Leu Ala Thr Asp
1   5   10   15

Ser Tyr Lys Val Thr His Tyr Lys Gln Tyr Pro Pro Asn Thr Ser Lys
            20   25   30

Val Tyr Ser Tyr Phe Glu Cys Arg Glu Lys Lys Thr Glu Asn Ser Lys
        35   40   45

Leu Arg Lys Val Lys Tyr Glu Glu Thr Val Phe Tyr Gly Leu Gln Tyr
    50   55   60

Ile Leu Asn Lys Tyr Leu Lys Gly Lys Val Val Thr Lys Glu Lys Ile
65   70   75   80

Gln Glu Ala Lys Asp Val Tyr Lys Glu His Phe Gln Asp Asp Val Phe

---

Leu Phe Leu Gly Ala Asp Gly Gly Cys Ile Thr Arg Gln Asp Leu
    530   535   540   560

Pro Lys Asp Cys Phe Ile Ile Tyr Gln Gly His His Gly Asp Val Gly
545   550   555   560

Ala Pro Ile Ala Asp Val Ile Leu Pro Gly Ala Ala Tyr Thr Glu Lys
        565   570   575

Ser Ala Thr Tyr Val Asn Thr Glu Gly Arg Ala Gln Gln Thr Lys Val
        580   585   590

Ala Val Thr Pro Pro Gly Leu Ala Arg Glu Asp Trp Lys Ile Ile Arg
    595   600   605

Ala Leu Ser Glu Ile Ala Gly Met Thr Leu Pro Tyr Asp Thr Leu Asp
        610   615   620

Gln Val Arg Asn Arg Leu Glu Glu Phe Ser Pro Asn Leu Val Arg Tyr
625   630   635   640

Asp Asp Ile Glu Gly Ala Asn Tyr Phe Gln Gln Ala Asn Glu Leu Ser
        645   650   655

Lys Leu Val Asn Gln Leu Leu Ala Asp Pro Leu Val Pro Pro Gln
    660   665   670

Leu Thr Leu Lys Asp Phe Tyr Met Thr Asp Ser Ile Ser Arg Ala Ser
    675   680   685

Gln Thr Met Ala Lys Cys Val Lys Ala Val Thr Glu Gly Ala Gln Ala
    690   695   700

Val Glu Glu Pro Ser Ile Cys
705   710   715   720

Asn Glu Lys Gly Trp Asn Tyr Ile Leu Glu Lys Tyr Asp Gly His Leu
     85   90   95

Pro Ile Glu Ile Lys Ala Val Pro Glu Gly Phe Val Ile Pro Arg Gly
   100   105   110

5

Asn Val Leu Phe Thr Val Glu Asn Thr Asp Pro Glu Cys Tyr Trp Leu
   115   120   125

Thr Asn Trp Ile Glu Thr Ile Leu Val Gln Ser Trp Tyr Pro Ile Thr
   130   135   140

Val Ala Thr Asn Ser Arg Glu Gln Lys Lys Ile Leu Ala Lys Tyr Leu
   145   150   155   160

10

Leu Glu Thr Ser Gly Asn Leu Asp Gly Leu Glu Tyr Lys Leu His Asp
   165   170   175

Phe Gly Tyr Arg Gly Val Ser Ser Gln Glu Thr Ala Gly Ile Gly Ala
   180   185   190

15

Ser Ala His Leu Val Asn Phe Lys Gly Thr Asp Thr Val Ala Gly Leu
   195   200   205

Ala Leu Ile Lys Lys Tyr Tyr Gly Thr Lys Asp Pro Val Pro Gly Tyr
   210   215   220

20

Ser Val Pro Ala Glu Ala His Ser Thr Ile Thr Ala Trp Gly Lys Asp
   225   230   235   240

His Glu Lys Asp Ala Phe Glu His Ile Val Thr Gln Phe Ser Ser Val
   245   250   255

Pro Val Ser Val Val Ser Asp Ser Tyr Asp Ile Tyr Asn Ala Cys Glu
   260   265   270

Lys Ile Trp Gly Glu Asp Leu Arg His Leu Ile Val Ser Arg Ser Thr
   275   280   285

Gln Ala Pro Leu Ile Ile Arg Asp Ser Gly Asn Pro Leu Asp Thr
   290   295   300

5

Val Leu Lys Val Leu Glu Ile Leu Gly Lys Lys Phe Pro Val Thr Glu
   305   310   315   320

Asn Ser Lys Gly Tyr Lys Leu Leu Pro Pro Tyr Arg Val Ile Gln
   325   330   335

10

Gly Asp Gly Val Asp Ile Asn Thr Leu Gln Glu Ile Val Glu Gly Met
   340   345   350

Lys Gln Lys Met Trp Ser Ile Glu Asn Ile Ala Phe Gly Ser Gly Gly
   355   360   365

Gly Leu Leu Gln Lys Leu Thr Arg Asp Leu Asn Cys Ser Phe Lys
   370   375   380

15

Cys Ser Tyr Val Val Asn Gly Leu Gly Ile Asn Val Phe Lys Asp
   385   390   395   400

Pro Val Ala Asp Pro Asn Lys Arg Ser Lys Gly Arg Leu Ser Leu
   405   410   415

20

His Arg Thr Pro Ala Gly Asn Phe Val Thr Leu Glu Glu Gly Lys Gly
   420   425   430

Asp Leu Glu Glu Tyr Gly Gln Asp Leu Leu His Thr Val Phe Lys Asn
   435   440   445

Gly Lys Val Thr Lys Ser Tyr Ser Phe Asp Glu Ile Arg Lys Asn Ala
   450   455   460

```
                65              70              75              80
Arg Lys Cys Met Thr Thr Val Ser Trp Asp Gly Asp Lys Leu Gln Cys
                                85              90              95
Val Gln Lys Gly Glu Lys Gly Gly Arg Gly Trp Gln Trp Ile Glu
        100             105             110
Gly Asp Glu Leu His Leu Glu Met Arg Val Glu Gly Val Val Cys Lys
        115             120             125
Gln Val Phe Lys Lys Val Gln
        130             135
```

```
<210> 45
<211> 544
<212> PRT
<213> Homo sapiens
<220>
<221> T-complex protein 1, gamma subunit
<222> (1)..(544)
<223> Accession No. as of 09 Dec 2002: P49368
<400> 45
```

```
Met Gly His Arg Pro Val Leu Val Leu Ser Gln Asn Thr Lys Arg Glu
1               5               10              15
Ser Gly Arg Lys Val Gln Ser Gly Asn Ile Asn Ala Ala Lys Thr Ile
```

```
                465             470             475             480
Gln Leu Asn Ile Glu Glu Leu Glu Ala Ala His His
                                485             490
```

```
<210> 44
<211> 135
<212> PRT
<213> Homo sapiens
<220>
<221> Retinol-binding protein I, cellular
<222> (1)..(135)
<223> Accession No. as of 09 Dec 2002: P09455
<400> 44
```

```
Met Pro Val Asp Phe Thr Gly Tyr Trp Lys Met Leu Val Asn Glu Asn
1               5               10              15
Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys
        20              25              30
Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp
        35              40              45
His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp
50              55              60
Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp
```

Ala Asp Ile Arg Thr Cys Leu Gly Pro Lys Ser Met Met Lys Met
    20   25   30

    35   40   45
Leu Leu Asp Pro Met Gly Gly Ile Val Met Thr Asn Asp Gly Asn Ala
5   50   55   60

Ile Leu Arg Glu Ile Gln Val Gln His Pro Ala Ala Lys Ser Met Ile
65   70   75   80

Glu Ile Ser Arg Thr Gln Asp Glu Glu Val Gly Asp Gly Thr Thr Ser
85   90   95

10 Val Ile Ile Leu Ala Gly Glu Met Leu Ser Val Ala Glu His Phe Leu
100   105   110

Glu Gln Gln Met His Pro Thr Val Ile Ser Ala Tyr Arg Lys Ala
115   120   125

Leu Asp Asp Met Ile Ser Thr Leu Lys Lys Ile Ser Ile Pro Val Asp
130   135   140

15 Ile Ser Asp Ser Asp Met Met Leu Asn Ile Ile Asn Ser Ser Ile Thr
145   150   155   160

Thr Lys Ala Ile Ser Arg Trp Ser Ser Leu Ala Cys Asn Ile Ala Leu
165   170   175

20 Asp Ala Val Lys Met Val Gln Phe Glu Glu Asn Gly Arg Lys Glu Ile
180   185   190

Asp Ile Lys Lys Tyr Ala Arg Val Glu Lys Ile Pro Gly Gly Ile Ile
195   200   205

Glu Asp Ser Cys Val Leu Arg Gly Val Met Ile Asn Lys Asp Val Thr

    210   215   220
His Pro Arg Met Arg Arg Tyr Ile Lys Asn Pro Arg Ile Val Leu Leu
    225   230   235   240
Asp Ser Ser Leu Glu Tyr Lys Lys Gly Glu Ser Gln Thr Asp Ile Glu
5   245   250   255
Ile Thr Arg Glu Glu Asp Phe Thr Arg Ile Leu Gln Met Glu Glu Glu
260   265   270
Tyr Ile Gln Gln Leu Cys Glu Asp Ile Ile Gln Leu Lys Pro Asp Val
275   280   285
10 Val Ile Thr Glu Lys Gly Ile Ser Asp Leu Ala Gln His Tyr Leu Met
290   295   300
Arg Ala Asn Ile Thr Ala Ile Arg Arg Val Arg Lys Thr Asp Asn Asn
305   310   315   320
Arg Ile Ala Arg Ala Cys Gly Ala Arg Ile Val Ser Arg Pro Glu Glu
15   325   330   335
Leu Arg Glu Asp Asp Val Gly Thr Gly Ala Gly Leu Leu Glu Ile Lys
340   345   350
Lys Ile Gly Asp Glu Tyr Phe Thr Phe Ile Thr Asp Cys Lys Asp Pro
355   360   365
20 Lys Ala Cys Thr Ile Leu Leu Arg Gly Ala Ser Lys Glu Ile Leu Ser
370   375   380
Glu Val Glu Arg Asn Leu Gln Asp Ala Met Gln Val Cys Arg Asn Val
385   390   395   400
Leu Leu Asp Pro Gln Leu Val Pro Gly Gly Gly Ala Ser Glu Met Ala

<221> Placental ribonuclease inhibitor

<222> (1)..(461)

<223> Accession No. as of 09 Dec 2002: P13489

<400> 46

Met Ser Leu Asp Ile Gln Ser Leu Asp Ile Gln Cys Glu Glu Leu Ser
1   5   10   15

Asp Ala Arg Trp Ala Glu Leu Leu Pro Leu Leu Gln Gln Cys Gln Val
20   25   30

Val Arg Leu Asp Asp Cys Gly Leu Thr Glu Ala Arg Cys Lys Asp Ile
35   40   45

Ser Ser Ala Leu Arg Val Asn Pro Ala Leu Ala Glu Leu Asn Leu Arg
50   55   60

Ser Asn Glu Leu Gly Asp Val Gly Val His Cys Val Leu Gln Gly Leu
65   70   75   80

Gln Thr Pro Ser Cys Ile Gln Lys Leu Ser Leu Gln Asn Cys Cys
85   90   95

Leu Thr Gly Ala Gly Cys Gly Val Leu Ser Ser Thr Leu Arg Thr Leu
100   105   110

Pro Thr Leu Gln Glu Leu His Leu Ser Asp Asn Leu Leu Gly Asp Ala
115   120   125

Gly Leu Gln Leu Leu Cys Glu Gly Leu Leu Asp Pro Gln Cys Arg Leu
130   135   140

Glu Lys Leu Gln Leu Glu Tyr Cys Ser Leu Ser Ala Ala Ser Cys Glu

Val Ala His Ala Leu Thr Glu Lys Ser Lys Met Thr Gly Val Glu
405   410   415

Gln Trp Pro Tyr Arg Ala Val Ala Gln Ala Leu Glu Val Ile Pro Arg
420   425   430

435   440   445

Thr Leu Ile Gln Asn Cys Gly Ala Ser Thr Ile Arg Leu Leu Thr Ser
450   455   460

Leu Arg Ala Lys His Thr Gln Glu Asn Cys Glu Thr Trp Gly Val Asn
465   470   475   480

Gly Glu Thr Gly Thr Leu Val Asp Met Lys Glu Leu Gly Ile Trp Glu
485   490   495

Pro Leu Ala Val Lys Leu Gln Thr Tyr Lys Thr Ala Val Glu Thr Ala
500   505   510

Val Leu Leu Arg Ile Asp Asp Ile Val Ser Gly His Lys Lys Lys Lys
515   520   525

Gly Asp Asp Gln Ser Arg Gln Gly Gly Ala Pro Asp Ala Gly Gln Glu
530   535   540

<210> 46

<211> 461

<212> PRT

<213> Homo sapiens

<220>

```
                       145            150            155            160
   Pro Leu Ala Ser Val Arg Leu Ala Lys Pro Asp Phe Lys Glu Leu Thr
                              165            170            175
   Val Ser Asn Asn Asp Ile Asn Glu Ala Gly Val Arg Val Leu Cys Gln
5                             180            185            190
   Gly Leu Lys Asp Ser Pro Cys Gln Leu Glu Ala Leu Lys Leu Glu Ser
                              195            200            205
   Cys Gly Val Thr Ser Asp Asn Cys Arg Asp Leu Cys Gly Ile Val Ala
                              210            215            220
   Ser Lys Ala Ser Leu Arg Glu Leu Ala Leu Gly Ser Asn Lys Leu Gly
10                            225            230            235            240
   Asp Val Gly Met Ala Glu Leu Cys Pro Gly Leu Leu His Pro Ser Ser
                              245            250            255
   Arg Leu Arg Thr Leu Trp Ile Trp Glu Cys Gly Ile Thr Ala Lys Gly
15                            260            265            270
   Cys Gly Asp Leu Cys Arg Val Leu Arg Ala Lys Glu Ser Leu Lys Glu
                              275            280            285
   Leu Ser Leu Ala Gly Asn Glu Leu Gly Asp Glu Gly Ala Arg Leu Leu
                              290            295            300
   Cys Glu Thr Leu Leu Glu Pro Gly Cys Gln Leu Glu Ser Leu Trp Val
20                            305            310            315            320
   Lys Ser Cys Ser Phe Thr Ala Ala Cys Cys Ser His Phe Ser Ser Val
                              325            330            335
   Leu Ala Gln Asn Arg Phe Leu Leu Glu Leu Gln Ile Ser Asn Asn Arg
```

```
                       340            345            350
   Leu Glu Asp Ala Gly Val Arg Glu Leu Cys Gln Gly Leu Gly Gln Pro
                              355            360            365
   Gly Ser Val Leu Arg Val Leu Trp Leu Ala Asp Cys Asp Val Ser Asp
5                             370            375            380
   Ser Ser Cys Ser Ser Leu Ala Ala Thr Leu Leu Ala Asn His Ser Leu
                              385            390            395            400
   Arg Glu Leu Asp Leu Ser Asn Asn Cys Leu Gly Asp Ala Gly Ile Leu
10                            405            410            415
   Gln Leu Val Glu Ser Val Arg Gln Pro Gly Cys Leu Leu Glu Gln Leu
                              420            425            430
   Val Leu Tyr Asp Ile Tyr Trp Ser Glu Glu Met Glu Asp Arg Leu Gln
                              435            440            445
   Ala Leu Glu Lys Asp Lys Pro Ser Leu Arg Val Ile Ser
15                            450            455            460


   <210> 47
   <211> 317
20 <212> PRT
   <213> Homo sapiens
   <220>
   <221> Guanine nucleotide-binding protein beta subunit-like protein
   12.3
```

<222> (1)..(317)

<223> Accession No. as of 09 Dec 2002: P25388

<400> 47

Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly
1   5   10   15

Trp Val Thr Gln Ile Ala Thr Pro Gln Phe Pro Asp Met Ile Leu
            20   25   30

Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp
10   35   40   45

Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His
        50   55   60

Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser
65   70   75   80

Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr
15   85   90   95

Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala
            100   105   110

Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr
20   115   120   125

Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp
        130   135   140

Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser
145   150   155   160

Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val
                            165   170   175

Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr
                            180   185   190

Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala
5   195   200   205

Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly
                    210   215   220

Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys
10 225   230   235   240

Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile
                    245   250   255

Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln
                    260   265   270

Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser
15   275   280   285

Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp
                    290   295   300

Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg
20 305   310   315

<210> 48

<211> 172

```
<212> PRT

<213> Homo sapiens

<220>

<221> Myosin regulatory light chain 2

5    <222> (1)..(172)

<223> Accession No. as of 10 Dec 2002: P24844

<400> 48


Met Ser Ser Lys Arg Ala Lys Ala Thr Thr Lys Lys Arg Pro Gln
10    1               5                   10                  15

Arg Ala Thr Ser Asn Val Phe Ala Met Phe Asp Gln Ser Gln Ile Gln
                20                  25                  30

Glu Phe Lys Glu Ala Phe Asn Met Ile Asp Gln Asn Arg Asp Gly Phe
15        35                  40                  45

Ile Asp Lys Glu Asp Leu His Asp Met Leu Ala Ser Leu Gly Lys Asn
        50                  55                  60

Pro Thr Asp Glu Tyr Leu Glu Gly Met Met Ser Glu Ala Pro Gly Pro
20    65                  70                  75                  80

Ile Asn Phe Thr Met Phe Leu Thr Met Phe Gly Glu Lys Leu Asn Gly
                    85                  90                  95

Thr Asp Pro Glu Asp Val Ile Arg Asn Ala Phe Ala Cys Phe Asp Glu
                    100                 105                 110

Glu Ala Ser Gly Phe Ile His Glu Asp His Leu Arg Glu Leu Leu Thr
            115                 120                 125
```

```
Thr Met Gly Asp Arg Phe Thr Asp Glu Val Asp Glu Met Tyr Arg
                130                 135                 140

Glu Ala Pro Ile Asp Lys Lys Gly Asn Phe Asn Tyr Val Glu Phe Thr
145                 150                 155                 160

5    Arg Ile Leu Lys His Gly Ala Lys Asp Lys Asp Asp
                165                 170


<210> 49

10    <211> 114

<212> PRT

<213> Homo sapiens

<220>

<221> Calgranulin B

15    <222> (1)..(114)

<223> Accession No. as of 10 Dec 2002: P06702

<400> 49


Met Thr Cys Lys Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile
20    1               5                   10                  15

Asn Thr Phe His Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu
                    20                  25                  30

Asn Gln Gly Glu Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe
            35                  40                  45
```

```
Leu Lys Glu Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu
                    50                  55              60
Asp Leu Asp Thr Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Ile
                    65                  70              75              80
  5  Met Leu Met Ala Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu
                    85                  90              95
Gly Asp Glu Gly Gly His His His Lys Pro Gly Leu Gly Gly Gly
                    100                 105             110
Thr Pro

 10


 15  <210> 50
     <211> 348
     <212> PRT
     <213> Homo sapiens
     <220>
     <221> Macrophage capping protein
 20  <222> (1)..(348)
     <223> Accession No. as of 10 Dec 2002: P40121

     <400> 50

Met Tyr Thr Ala Ile Pro Gln Ser Gly Ser Pro Phe Pro Gly Ser Val
  1                5                   10              15
```

```
Gln Asp Pro Gly Leu His Val Trp Arg Val Glu Lys Leu Lys Pro Val
                    20                  25              30
Pro Val Ala Gln Glu Asn Gln Gly Val Phe Phe Ser Gly Asp Ser Tyr
                    35                  40              45
  5  Leu Val Leu His Asn Gly Pro Glu Glu Val Ser His Leu His Leu Trp
                    50                  55              60
Ile Gly Gln Ser Ser Arg Asp Glu Gln Gly Ala Cys Ala Val Leu
                    65                  70              75              80
Ala Val His Leu Asn Thr Leu Leu Gly Glu Arg Pro Val Gln His Arg
                    85                  90              95
 10  Glu Val Gln Gly Asn Glu Ser Asp Leu Phe Met Ser Tyr Phe Pro Arg
                    100                 105             110
Gly Leu Lys Tyr Gln Glu Gly Gly Val Glu Ser Ala Phe His Lys Thr
                    115                 120             125
 15  Ser Thr Gly Ala Pro Ala Ala Ile Lys Leu Tyr Gln Val Lys Gly
                    130                 135             140
Lys Asn Ile Arg Ala Thr Glu Arg Ala Leu Asn Trp Asp Ser Phe
                    145                 150             155             160
Asn Thr Gly Asp Cys Phe Ile Leu Asp Leu Gly Gln Asn Ile Phe Ala
                    165                 170             175
 20  Trp Cys Gly Lys Ser Asn Ile Leu Glu Arg Asn Lys Ala Arg Asp
                    180                 185             190
Leu Ala Leu Ala Ile Arg Asp Ser Glu Arg Gln Gly Lys Ala Gln Val
                    195                 200             205
```

```
      Glu Ile Val Thr Asp Gly Glu Glu Pro Ala Glu Met Ile Gln Val Leu
                      210                 215                 220

      Gly Pro Lys Pro Ala Leu Lys Glu Gly Asn Pro Glu Glu Asp Leu Thr
                      225                 230                 235                 240

  5   Ala Asp Lys Ala Asn Ala Gln Ala Ala Ala Leu Tyr Lys Val Ser Asp
                      245                 250                 255

      Ala Thr Gly Gln Met Asn Asn Leu Thr Lys Val Ala Asp Ser Pro Phe
                      260                 265                 270

      Ala Leu Glu Leu Ile Ser Asp Asp Cys Phe Val Leu Asp Asn Gly
  10                  275                 280                 285

      Leu Cys Gly Lys Ile Tyr Ile Trp Trp Lys Gly Arg Arg Lys Ala Asn Glu Lys
                      290                 295                 300

      Glu Arg Gln Ala Ala Leu Gln Val Ala Glu Gly Phe Ile Ser Arg Met
                      305                 310                 315                 320

  15  Gln Tyr Ala Pro Asn Thr Gln Val Glu Ile Leu Pro Gln Gly Arg Glu
                      325                 330                 335

      Ser Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Lys
                      340                 345

  20

      <210> 51
      <211> 346
      <212> PRT
      <213> Homo sapiens
```

```
      <220>

      <221> Annexin I

      <222> (1)..(346)

      <223> Accession No. as of 10 Dec 2002: P04083

  5   <400> 51

      Met Ala Met Val Ser Glu Gly Phe Leu Lys Gln Ala Trp Phe Ile Glu Asn
      1               5                   10                  15

      Glu Glu Gln Glu Tyr Val Gln Thr Val Lys Ser Ser Lys Gly Gly Pro
  10                  20                  25                  30

      Gly Ser Ala Val Ser Pro Tyr Pro Thr Phe Asn Pro Ser Ser Asp Val
                      35                  40                  45

      Ala Ala Leu His Lys Ala Ile Met Val Lys Gly Val Asp Glu Ala Thr
                      50                  55                  60

  15  Ile Ile Asp Ile Leu Thr Lys Arg Asn Asn Ala Gln Arg Gln Gln Ile
      65                  70                  75                  80

      Lys Ala Ala Tyr Leu Gln Glu Thr Gly Lys Pro Leu Asp Glu Thr Leu
                      85                  90                  95

      Lys Lys Ala Leu Thr Gly His Leu Glu Glu Val Val Leu Ala Leu Leu
  20                  100                 105                 110

      Lys Thr Pro Ala Gln Phe Asp Ala Asp Glu Leu Arg Ala Ala Met Lys
                      115                 120                 125

      Gly Leu Gly Thr Asp Glu Asp Thr Leu Ile Glu Ile Leu Ala Ser Arg
                      130                 135                 140
```

Thr Asn Lys Glu Ile Arg Asp Ile Asn Arg Val Tyr Arg Glu Glu Leu
145   150   155   160

Lys Arg Asp Leu Ala Lys Asp Ile Thr Ser Asp Thr Ser Gly Asp Phe
165   170   175

5   Arg Asn Ala Leu Leu Ser Leu Ala Lys Gly Asp Arg Ser Glu Asp Phe
180   185   190

Gly Val Asn Glu Asp Leu Ala Asp Ser Asp Ala Arg Ala Leu Tyr Glu
195   200   205

Ala Gly Glu Arg Arg Lys Gly Thr Asp Val Asn Val Phe Asn Thr Ile
10   210   215   220

Leu Thr Thr Arg Ser Tyr Pro Gln Leu Arg Arg Val Phe Gln Lys Tyr
225   230   235   240

Thr Lys Tyr Ser Lys His Asp Met Asn Lys Val Leu Asp Leu Glu Leu
245   250   255

15   Lys Gly Asp Ile Glu Lys Cys Leu Thr Ala Ile Val Lys Cys Ala Thr
260   265   270

Ser Lys Pro Ala Phe Phe Ala Glu Lys Leu His Gln Ala Met Lys Gly
275   280   285

Val Gly Thr Arg His Lys Ala Leu Ile Met Ile Arg Ile Met Val Ser Arg Ser
20   290   295   300

Glu Ile Asp Met Asn Asp Ile Lys Ala Phe Tyr Gln Lys Met Tyr Gly
305   310   315   320

Ile Ser Leu Cys Gln Ala Ile Leu Asp Glu Thr Lys Gly Asp Tyr Glu
325   330   335

Lys Ile Leu Val Ala Leu Cys Gly Gly Asn
340   345

5   <210> 52

<211> 469

<212> PRT

<213> Homo sapiens

<220>

10   <221> Keratin, type II cytoskeletal 7

<222> (1)..(469)

<223> Accession No. as of 10 Dec 2002: P08729

<400> 52

15   Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala
1   5   10   15

Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly
20   25   30

Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg
35   40   45

20   Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg
50   55   60

Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Asp Ala
65   70   75   80

```
Asp Pro Ser Leu Gln Arg Val Arg Gln Glu Ser Glu Gln Ile Lys
                        85                  90                  95

Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu
                       100                 105                 110

5 Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu
                       115                 120                 125

Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala Gln
                       130                 135                 140

Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Leu Gln Val Asp Gly Gly
10  145                 150                 155                 160

Arg Leu Glu Gln Gly Leu Arg Thr Met Gln Asp Val Val Glu Asp Phe
                       165                 170                 175

Lys Asn Lys Tyr Glu Asp Ile Asn Arg Arg Thr Ala Ala Glu Asn
                       180                 185                 190

15 Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser Lys
                       195                 200                 205

Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asn Asp Glu Ile Asn Phe
                       210                 215                 220

Leu Arg Thr Leu Asn Glu Thr Glu Leu Thr Glu Leu Gln Ser Gln Ile
20 225                 230                 235                 240

Ser Asp Thr Ser Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp
                       245                 250                 255

Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met Ala
                       260                 265                 270
```

```
Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe Glu
                       275                 280                 285

Thr Leu Gln Ala Gln Ala Gly His Gly Asp Asp Leu Arg Asn Thr
                       290                 295                 300

5 Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln Ala
                       305                 310                 315                 320

Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala Ile
                       325                 330                 335

Ala Glu Ala Glu Glu Arg Gly Glu Leu Ala Leu Lys Asp Ala Arg Ala
10                     340                 345                 350

Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met
                       355                 360                 365

Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu Ala
                       370                 375                 380

15 Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu
                       385                 390                 395                 400

Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Val Asn Ile Ser Val Met
                       405                 410                 415

Asn Ser Thr Gly Gly Ser Ser Gly Gly Ile Gly Leu Thr Leu
20                     420                 425                 430

Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ala Gly
                       435                 440                 445

Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Arg
                       450                 455                 460
```

Arg Ser Ala Arg Asp
465

<210> 53
<211> 836
<212> PRT
<213> Homo sapiens
<220>
<221> Osteoblast specific factor 2 precursor
<222> (1)..(836)
<223> Accession No. as of 10 Dec 2002: Q15063
<400> 53

```
Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Leu Ile Val
1               5                   10                  15
Asn Pro Ile Asn Ala Asn His Tyr Asp Lys Ile Leu Ala His Ser
            20                  25                  30
Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
        35                  40                  45
Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
    50                  55                  60
Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys
65                  70                  75                  80
```

```
     Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
                         85                  90                  95
     Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
                         100                 105                 110
5    Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
                         115                 120                 125
     Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn
                         130                 135                 140
10   Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu
         145                 150                 155                 160
     Leu Leu Asn Ala Leu His Ser His Met Ile Asn Lys Arg Met Leu Thr
                         165                 170                 175
     Lys Asp Leu Lys Asn Gly Met Ile Ile Pro Ser Met Tyr Asn Asn Leu
                         180                 185                 190
15   Gly Leu Phe Ile Asn His Tyr Pro Asn Gly Val Val Thr Val Asn Cys
                         195                 200                 205
     Ala Arg Ile Ile His Gly Asn Gln Ile Ala Thr Asn Gly Val Val His
                         210                 215                 220
     Val Ile Asp Arg Val Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe
20       225                 230                 235                 240
     Ile Glu Ala Glu Asp Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr
                         245                 250                 255
     Ser Asp Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe
                         260                 265                 270
```

Ala Pro Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu
            275   280   285

Arg Phe Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His
            290   295   300

5   Ile Leu Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val
            305   310   315   320

Phe Glu Thr Leu Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp
            325   330   335

10   Ser Ile Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val
            340   345   350

Thr Asn Gly Val Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp
            355   360   365

Ser Ala Lys Gln Val Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe
            370   375   380

15   Thr Asp Leu Val Ala Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp
            385   390   395   400

Gly Glu Tyr Thr Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp
            405   410   415

Thr Leu Ser Met Val Gln Arg Leu Leu Lys Leu Ile Leu Gln Asn His
            420   425   430

20   Ile Leu Lys Val Lys Val Gly Leu Asn Glu Leu Tyr Asn Gly Gln Ile
            435   440   445

Leu Glu Thr Ile Gly Gly Lys Gln Leu Arg Val Phe Val Tyr Arg Thr
            450   455   460

Ala Val Cys Ile Glu Asn Ser Cys Met Ser Glu Lys Gly Ser Lys Gln Gly
            465   470   475   480

Arg Asn Gly Ala Ile His Ile Phe Arg Glu Ile Ile Lys Pro Ala Glu
            485   490   495

5   Lys Ser Leu His Glu Lys Leu Lys Gln Asp Lys Arg Phe Ser Thr Phe
            500   505   510

Leu Ser Leu Glu Ala Ala Asp Leu Lys Glu Leu Leu Gln Pro
            515   520   525

Gly Asp Trp Thr Leu Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met
            530   535   540

10   Thr Ser Glu Glu Lys Glu Leu Ile Arg Asp Lys Asn Ala Leu Gln
            545   550   555   560

Asn Ile Ile Leu Tyr His Leu Thr Pro Gly Val Phe Ile Gly Lys Gly
            565   570   575

15   Phe Glu Pro Gly Val Thr Asn Ile Leu Lys Thr Thr Gln Gly Ser Lys
            580   585   590

Ile Phe Leu Lys Glu Val Asn Asp Thr Leu Leu Val Asn Glu Leu Lys
            595   600   605

Ser Lys Glu Ser Asp Ile Met Thr Thr Asn Gly Val Ile His Val
            610   615   620

20   Asp Lys Leu Leu Tyr Pro Ala Asp Thr Pro Val Gly Asn Asp Gln Leu
            625   630   635   640

Leu Glu Ile Leu Asn Lys Leu Ile Lys Tyr Ile Gln Ile Lys Phe Val
            645   650   655

```
Arg Gly Ser Thr Phe Lys Glu Ile Pro Val Thr Val Tyr Thr Thr Lys
                    660                 665                 670

Ile Ile Thr Lys Val Val Glu Pro Lys Ile Lys Val Ile Glu Gly Ser
           675                 680                 685

Leu Gln Pro Ile Ile Lys Thr Glu Gly Pro Thr Leu Thr Lys Val Lys
                    690                 695                 700

Ile Glu Gly Glu Pro Glu Phe Arg Leu Ile Lys Glu Gly Glu Thr Ile
                705             710                 715                 720

Thr Glu Val Ile His Gly Glu Pro Ile Ile Lys Tyr Thr Lys Ile
                    725                 730                 735

Ile Asp Gly Val Pro Val Glu Ile Thr Glu Lys Glu Thr Arg Glu Glu
                    740                 745                 750

Arg Ile Ile Gly Pro Glu Ile Lys Tyr Thr Thr Arg Ile Ser Thr Gly
                    755                 760                 765

Gly Gly Thr Glu Glu Thr Leu Lys Lys Leu Leu Gln Glu Glu Val
                    770                 775                 780

Thr Lys Val Thr Lys Phe Ile Glu Gly Gly His Leu Phe Glu
                785             790                 795                 800

Asp Glu Glu Ile Lys Arg Leu Leu Gln Gly Asp Thr Pro Val Lys
                    805                 810                 815

Leu Gln Ala Asn Lys Lys Val Gln Gly Ser Arg Arg Arg Leu Arg Glu
                    820                 825                 830

Gly Arg Ser Gln
                    835
```

<210> 54
<211> 687
<212> PRT
<213> Homo sapiens
<220>
<221> Protein-glutamine gamma-glutamyltransferase
<222> (1)..(687)
<223> Accession No. P21980
<400> 54

```
Met Ala Glu Glu Leu Val Leu Glu Arg Cys Asp Leu Glu Leu Glu Thr
1               5                   10                  15

Asn Gly Arg Asp His His Thr Ala Asp Leu Cys Arg Glu Lys Leu Val
                20                  25                  30

Val Arg Arg Gly Gln Pro Phe Trp Leu Thr Leu His Phe Glu Gly Arg
                35                  40                  45

Asn Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
                50                  55                  60

Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
65                  70                  75                  80

Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
                85                  90                  95
```

Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
              100   105   110

Gly Leu Tyr Arg Leu Ser Leu Ala Ser Thr Gly Tyr Gln Gly Ser
      115   120   125

5 Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
           130   135   140

Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Arg Gln Glu Tyr Val
  145   150   155   160

Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
      165   170   175

10 Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile
           180   185   190

Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn Ala Gly
      195   200   205

15 Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg Val Val
           210   215   220

Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
  225   230   235   240

Trp Asp Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp Ile Gly
      245   250   255

20 Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val
           260   265   270

Lys Tyr Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
  275   280   285

Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
           290   295   300

His Asp Gln Asn Ser Asn Leu Ile Glu Tyr Arg Asn Glu Phe
  305   310   315   320

5 Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe His Cys
           325   330   335

Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu
      340   345   350

Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr
      355   360   365

10 Tyr Cys Cys Gly Pro Val Pro Val Arg Ala Ile Lys Glu Gly Asp Leu
           370   375   380

Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
  385   390   395   400

15 Val Val Asp Trp Ile Gln Gln Asp Asp Gly Ser Val His Lys Ser Ile
           405   410   415

Asn Arg Ser Leu Ile Val Gly Leu Lys Ile Ser Thr Lys Ser Val Gly
      420   425   430

Arg Asp Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro Glu Gly
      435   440   445

20 Ser Ser Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu Asn Lys
           450   455   460

Leu Ala Glu Lys Glu Glu Thr Gly Met Ala Met Arg Ile Arg Val Gly
  465   470   475   480

```
Gln Ser Met Asn Met Gly Ser Asp Val Phe Ala His Ile Thr
                485                 490                 495

Asn Asn Thr Ala Glu Glu Tyr Val Cys Arg Leu Leu Cys Ala Arg
                500                 505                 510

Thr Val Ser Tyr Asn Gly Ile Leu Gly Pro Glu Cys Gly Thr Lys Tyr
                515                 520                 525

Leu Leu Asn Leu Asn Leu Glu Pro Phe Ser Glu Lys Ser Val Pro Leu
                530                 535                 540

Cys Ile Leu Tyr Glu Lys Tyr Arg Asp Cys Leu Thr Glu Ser Asn Leu
                545                 550                 555                 560

Ile Lys Val Arg Ala Leu Leu Val Glu Pro Val Ile Asn Ser Tyr Leu
                565                 570                 575

Leu Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg
                580                 585                 590

Ile Leu Gly Glu Pro Lys Gln Lys Arg Lys Leu Val Ala Glu Val Ser
                595                 600                 605

Leu Gln Asn Pro Leu Pro Val Ala Leu Glu Gly Cys Thr Phe Thr Val
                610                 615                 620

Glu Gly Ala Gly Leu Thr Glu Glu Gln Lys Thr Val Glu Ile Pro Asp
                625                 630                 635                 640

Pro Val Glu Ala Gly Glu Glu Val Lys Val Arg Met Asp Leu Leu Pro
                645                 650                 655

Leu His Met Gly Leu His Lys Leu Val Asn Phe Glu Ser Asp Lys
                660                 665                 670
```

```
Leu Lys Ala Val Lys Gly Phe Arg Asn Val Ile Ile Gly Pro Ala
                675                 680                 685
```

<210> 55
<211> 204
<212> PRT
<213> Homo sapiens
<220>
<221> Rho GDP-dissociation inhibitor 1
<222> (1)..(204)
<223> Accession No. as of 10 Dec 2002: P52565
<400> 55

```
Met Ala Glu Gln Glu Pro Thr Ala Glu Gln Leu Ala Gln Ile Ala Ala
1               5                   10                  15

Glu Asn Glu Glu Asp Glu His Ser Val Asn Tyr Lys Pro Pro Ala Gln
                20                  25                  30

Lys Ser Ile Gln Glu Ile Gln Glu Leu Asp Lys Asp Asp Glu Ser Leu
                35                  40                  45

Arg Lys Tyr Lys Glu Ala Leu Leu Gly Arg Val Ala Val Ser Ala Asp
                50                  55                  60

Pro Asn Val Pro Asn Val Val Val Thr Gly Leu Thr Leu Val Cys Ser
                65                  70                  75                  80
```

```
Ser Ala Pro Gly Pro Leu Glu Leu Asp Leu Thr Gly Asp Leu Glu Ser
                85                    90                    95

Phe Lys Gln Ser Phe Val Leu Lys Glu Gly Val Glu Tyr Arg Ile
                100                   105                   110

5   Lys Ile Ser Phe Arg Val Asn Arg Glu Ile Val Ser Gly Met Lys Tyr
                115                   120                   125

Ile Gln His Thr Tyr Arg Lys Gly Val Lys Ile Asp Lys Thr Asp Tyr
                130                   135                   140

10  Met Val Gly Ser Tyr Gly Pro Arg Ala Glu Tyr Glu Phe Leu Thr
        145                   150                   155                   160

Pro Val Glu Glu Ala Pro Lys Gly Met Leu Ala Arg Gly Ser Tyr Ser
                165                   170                   175

Ile Lys Ser Arg Phe Thr Asp Asp Lys Thr Asp His Leu Ser Trp
                180                   185                   190

15  Glu Trp Asn Leu Thr Ile Lys Asp Trp Lys Asp
                195                   200
```

<210> 56
<211> 492
20 <212> PRT
<213> Homo sapiens
<220>
<221> Fascin 2

<222> (1)..(492)
<223> Accession No. as of 29 August 2003: O14926
<400> 56

```
5   Met Pro Thr Asn Gly Leu His Gln Val Leu Lys Ile Gln Phe Gly Leu
    1                5                    10                   15

Val Asn Asp Thr Asp Arg Tyr Leu Thr Ala Glu Ser Phe Gly Phe Lys
                20                   25                   30

Val Asn Ala Ser Ala Pro Ser Leu Lys Arg Lys Gln Thr Trp Val Leu
10              35                   40                   45

Glu Pro Asp Pro Gly Gln Gly Thr Ala Val Leu Leu Arg Ser Ser His
                50                   55                   60

Leu Gly Arg Tyr Leu Ser Ala Glu Glu Asp Gly Arg Val Ala Cys Glu
65              70                   75                   80

15  Ala Glu Gln Pro Gly Arg Asp Cys Arg Phe Leu Val Leu Pro Gln Pro
                85                   90                   95

Asp Gly Arg Trp Val Leu Arg Ser Glu Pro His Gly Arg Phe Phe Gly
                100                  105                  110

Gly Thr Glu Asp Gln Leu Ser Cys Phe Ala Thr Ala Val Ser Pro Ala
20              115                  120                  125

Glu Leu Trp Thr Val His Leu Ala Ile His Pro Gln Ala His Leu Leu
                130                  135                  140

Ser Val Ser Arg Arg Tyr Val His Leu Cys Pro Arg Glu Asp Glu
                145                  150                  155                  160
```

```
Met Ala Asp Gly Asp Lys Asp Pro Trp Gly Val Asp Ala Leu Leu Thr
                165                 170                 175

Leu Ile Phe Arg Ser Arg Arg Tyr Cys Leu Ser Cys Asp Ser Arg
             180                 185                 190

Tyr Leu Arg Ser Asp Gly Arg Leu Val Trp Glu Pro Glu Pro Arg Ala
5                195                 200                 205

Cys Tyr Thr Leu Glu Phe Lys Ala Gly Lys Leu Ala Phe Lys Asp Cys
             210                 215                 220

Asp Gly His Tyr Leu Ala Pro Val Gly Pro Ala Gly Thr Leu Lys Ala
10    225                 230                 235                 240

Gly Arg Asn Thr Arg Pro Gly Lys Asp Glu Leu Phe Asp Leu Glu Glu
             245                 250                 255

Ser His Pro Gln Val Val Leu Val Ala Ala Asn His Arg Tyr Val Ser
             260                 265                 270

Val Arg Gln Gly Val Asn Val Ser Ala Asn Gln Asp Asp Glu Leu Asp
15           275                 280                 285

His Glu Thr Phe Leu Met Gln Ile Asp Gln Glu Thr Lys Lys Cys Thr
             290                 295                 300

Phe Tyr Ser Ser Thr Gly Tyr Trp Thr Val Thr His Gly Gly
20    305                 310                 315                 320

Ile His Ala Thr Ala Thr Gln Val Ser Ala Asn Thr Met Phe Glu Met
             325                 330                 335

Glu Trp Arg Gly Arg Arg Val Ala Leu Lys Ala Ser Asn Gly Arg Tyr
             340                 345                 350
```

```
Val Cys Met Lys Lys Asn Gly Gln Leu Ala Ala Ile Ser Asp Phe Val
                355                 360                 365

Gly Lys Asp Glu Glu Phe Thr Leu Lys Leu Ile Asn Arg Pro Ile Leu
             370                 375                 380

Val Leu Arg Gly Leu Asp Gly Phe Val Cys His His Arg Gly Ser Asn
5                385                 390                 395                 400

Gln Leu Asp Thr Asn Arg Ser Val Tyr Asp Val Phe His Leu Ser Phe
             405                 410                 415

Ser Asp Gly Ala Tyr Arg Ile Arg Gly Arg Asp Gly Gly Phe Trp Tyr
             420                 425                 430

Thr Gly Ser His Gly Ser Val Cys Ser Asp Gly Glu Arg Ala Glu Asp
10           435                 440                 445

Phe Val Phe Glu Phe Arg Glu Arg Gly Arg Leu Ala Ile Arg Ala Arg
             450                 455                 460

Ser Gly Lys Tyr Leu Arg Gly Gly Ala Ser Gly Leu Leu Arg Ala Asp
15           465                 470                 475                 480

Ala Asp Ala Pro Ala Gly Thr Ala Leu Trp Glu Tyr
             485                 490
20

<210> 57
<211> 165
<212> PRT
<213> Homo sapiens
```

<220>

<221> Destrin (Actin-depolymerizing factor) (ADF)

<222> (1)..(165)

<223> Accession No. as of 29 August 2003: P18282

<400> 57

```
Met Ala Ser Gly Val Gln Val Ala Asp Glu Val Cys Arg Ile Phe Tyr
1               5                   10                  15

Asp Met Lys Val Arg Lys Cys Ser Thr Pro Glu Glu Ile Lys Lys Arg
            20                  25                  30

Lys Lys Ala Val Ile Phe Cys Leu Ser Ala Asp Lys Lys Cys Ile Ile
        35                  40                  45

Val Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Val Thr Ile
    50                  55                  60

Thr Asp Pro Phe Lys His Phe Val Gly Met Leu Pro Glu Lys Asp Cys
65                  70                  75                  80

Arg Tyr Ala Leu Tyr Asp Ala Ser Phe Glu Thr Lys Glu Ser Arg Lys
                85                  90                  95

Glu Glu Leu Met Phe Phe Leu Trp Ala Pro Glu Leu Ala Pro Leu Lys
                100                 105                 110

Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Phe
            115                 120                 125

Gln Gly Ile Lys His Glu Cys Gln Ala Asn Gly Pro Glu Asp Leu Asn
        130                 135                 140
```

```
Arg Ala Cys Ile Ala Glu Lys Leu Gly Gly Ser Leu Ile Val Ala Phe
            145                 150                 155                 160

Glu Gly Cys Pro Val
            165
```

<210> 58

<211> 492

<212> PRT

<213> Homo sapiens

<220>

<221> Fascin

<222> (1)..(492)

<223> Accession No. as of 29 August 2003: Q16658

<400> 58

```
Thr Ala Asn Gly Thr Ala Glu Ala Val Gln Ile Gln Phe Gly Leu Ile
1               5                   10                  15

Asn Cys Gly Asn Lys Tyr Leu Thr Ala Glu Ala Phe Gly Phe Lys Val
            20                  25                  30

Asn Ala Ser Ala Ser Ser Leu Lys Lys Lys Gln Ile Trp Thr Leu Glu
            35                  40                  45

Gln Pro Pro Asp Glu Ala Gly Ser Ala Ala Val Cys Leu Arg Ser His
        50                  55                  60
```

```
Leu Gly Arg Tyr Leu Ala Ala Asp Lys Asp Gly Asn Val Thr Cys Glu
    65                  70                  75                  80

Arg Glu Val Pro Gly Asp Cys Arg Phe Leu Ile Val Ala His Asp
                85                  90                  95

Asp Gly Arg Trp Ser Leu Gln Ser Glu Ala His Arg Arg Tyr Phe Gly
 5                  100                 105                 110

Gly Thr Glu Asp Arg Leu Ser Cys Phe Ala Gln Thr Val Ser Pro Ala
                115                 120                 125

Glu Lys Trp Ser Val His Ile Ala Met His Pro Gln Val Asn Ile Tyr
10                  130                 135                 140

Ser Val Thr Arg Lys Arg Tyr Ala His Leu Ser Ala Arg Pro Ala Asp
                145                 150                 155                 160

Glu Ile Ala Val Asp Arg Asp Val Trp Gly Val Asp Ser Leu Ile
                165                 170                 175

Thr Leu Ala Phe Gln Asp Gln Arg Tyr Ser Val Gln Thr Ala Asp His
15                  180                 185                 190

Arg Phe Leu Arg His Asp Gly Arg Leu Val Ala Arg Pro Glu Pro Ala
                195                 200                 205

Thr Gly Tyr Thr Leu Glu Phe Arg Ser Gly Lys Val Ala Phe Arg Asp
20                  210                 215                 220

Cys Glu Gly Arg Tyr Leu Ala Pro Ser Gly Pro Ser Gly Thr Leu Lys
                225                 230                 235                 240

Ala Gly Lys Ala Thr Lys Val Gly Lys Asp Glu Leu Phe Ala Leu Glu
                245                 250                 255
```

```
Gln Ser Cys Ala Gln Val Val Leu Gln Ala Ala Asn Glu Arg Asn Val
                260                 265                 270

Ser Thr Arg Gln Gly Met Asp Leu Ser Ala Asn Gln Asp Glu Glu Thr
                275                 280                 285

Asp Gln Glu Thr Phe Gln Leu Glu Ile Asp Arg Asp Thr Lys Lys Cys
 5                  290                 295                 300

Ala Phe Arg Thr His Thr Gly Lys Tyr Trp Leu Thr Ala Thr Gly
                305                 310                 315                 320

Gly Val Gln Ser Thr Ala Ser Ser Lys Asn Ala Ser Cys Tyr Phe Asp
10                  325                 330                 335

Ile Glu Trp Arg Asp Arg Arg Ile Thr Leu Arg Ala Ser Asn Gly Lys
                340                 345                 350

Phe Val Thr Ser Lys Lys Asn Gly Gln Leu Ala Ala Ser Val Glu Thr
                355                 360                 365

Ala Gly Asp Ser Glu Leu Phe Leu Met Lys Leu Ile Asn Arg Pro Ile
15                  370                 375                 380

Ile Val Phe Arg Gly Glu His Gly Phe Ile Gly Cys Arg Lys Val Thr
                385                 390                 395                 400

Gly Thr Leu Asp Ala Asn Arg Ser Ser Tyr Asp Val Phe Gln Leu Glu
                405                 410                 415

Phe Asn Asp Gly Ala Tyr Asn Ile Lys Asp Ser Thr Gly Lys Tyr Trp
20                  420                 425                 430

Thr Val Gly Ser Asp Ser Ala Val Thr Ser Ser Gly Asp Thr Pro Val
                435                 440                 445
```

Asp Phe Phe Cys Asp Tyr Asn Lys Val Ala Ile Lys Val
450   455   460

Gly Gly Arg Tyr Leu Lys Asp His Ala Gly Val Leu Lys Ala Ser
465   470   475   480

Ala Glu Thr Val Asp Pro Ala Ser Leu Trp Glu Tyr
485   490

<210> 59
<211> 317
<212> PRT
<213> Homo sapiens

<220>
<221> Apo-E precursor
<222> (1)..(317)
<223> Accession No. as of 29 August 2003: P02649

<400> 59

Met Lys Val Leu Trp Ala Ala Leu Leu Val Thr Phe Leu Ala Gly Cys
1   5   10   15

Gln Ala Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu
20   25   30

Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu
35   40   45

Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln
50   55   60

Val Gln Glu Glu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala
65   70   75   80

Leu Met Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu
85   90   95

Glu Glu Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser
100   105   110

Lys Glu Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp
115   120   125

Val Cys Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu
130   135   140

Gly Gln Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg
145   150   155   160

Lys Leu Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg
165   170   175

Leu Ala Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu
180   185   190

Ser Ala Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val
195   200   205

Arg Ala Ala Thr Val Gly Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg
210   215   220

Ala Gln Ala Trp Gly Glu Arg Leu Arg Ala Arg Met Glu Glu Met Gly
225   230   235   240

```
Gly Thr Val Thr Val Arg Tyr Ala Pro Ser Glu Ala Gly Leu His Glu
                    20              25              30
Met Asp Ile Arg Tyr Asp Asn Met His Ile Pro Gly Ser Pro Leu Gln
                35              40              45
5   Phe Tyr Val Asp Tyr Val Asn Cys Gly His Val Thr Ala Tyr Gly Pro
            50              55              60
Gly Leu Thr His Gly Val Val Asn Lys Pro Ala Thr Phe Thr Val Asn
        65              70              75              80
Thr Lys Asp Ala Gly Glu Gly Gly Leu Ser Leu Ala Ile Glu Gly Pro
10      85              90              95
Ser Lys Ala Glu Ile Ser Cys Thr Asp Asn Gln Asp Gly Thr Cys Ser
                    100             105             110
Val Ser Tyr Leu Pro Val Leu Pro Gly Asp Tyr Ser Ile Leu Val Lys
                115             120             125
15  Tyr Asn Glu Gln His Val Pro Gly Ser Pro Phe Thr Ala Arg Val Thr
                130             135             140
Gly Asp Asp Ser Met Arg Met Ser His Leu Lys Val Gly Ser Ala Ala
                145             150             155             160
Asp Ile Pro Ile Asn Ile Ser Glu Thr Asp Leu Ser Leu Leu Thr Ala
20              165             170             175
Thr Val Val Pro Pro Ser Gly Arg Glu Glu Pro Cys Leu Leu Lys Arg
                    180             185             190
Leu Arg Asn Gly His Val Gly Ile Ser Phe Val Pro Lys Glu Thr Gly
                    195             200             205
```

```
Ser Arg Thr Arg Asp Leu Asp Glu Lys Glu Gln Val Ala Glu
                    245             250             255
Val Arg Ala Lys Leu Glu Glu Gln Ala Gln Gln Ile Arg Leu Gln Ala
                260             265             270
5   Glu Ala Phe Gln Ala Arg Leu Lys Ser Trp Phe Glu Pro Leu Val Glu
                275             280             285
Asp Met Gln Arg Gln Trp Ala Gly Leu Val Glu Lys Val Gln Ala Ala
                290             295             300
Val Gly Thr Ser Ala Ala Pro Val Pro Ser Asp Asn His
10      305             310             315

<210> 60
<211> 838
<212> PRT
<213> Homo sapiens
<220>
<221> hypothetical 88.6 kDa protein
<222> (1)..(838)
<223> Accession No. as of 29 August 2003: Q96C61
<400> 60

Met Pro Ser Gly Lys Val Ala Gln Pro Thr Ile Thr Asp Asn Lys Asp
1               5               10              15
```

```
     Glu His Leu Val His Val Lys Asn Gly Gln His Val Ala Ser Ser
                   210             215                 220

     Pro Ile Pro Val Val Ile Ser Gln Ser Glu Ile Gly Asp Ala Ser Arg
                   225             230             235             240

  5  Val Arg Val Ser Gly Gln Gly Leu His Glu Gly Thr Phe Glu Pro
                   245             250                 255

     Ala Glu Phe Ile Asp Thr Arg Asp Ala Gly Tyr Gly Gly Leu Ser
                   260             265                 270

     Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn Thr Glu Asp Leu
 10                275             280                 285

     Glu Asp Gly Thr Cys Arg Val Thr Tyr Cys Pro Thr Pro Gly Asn
                   290             295                 300

     Tyr Ile Ile Asn Ile Lys Phe Ala Asp Gln His Val Pro Gly Ser Pro
                   305             310             315             320

 15  Phe Ser Val Lys Val Thr Gly Glu Gly Arg Val Lys Glu Ser Ile Thr
                   325             330                 335

     Arg Arg Arg Ala Pro Ser Val Ala Asn Val Gly Ser His Cys Asp
                   340             345                 350

     Leu Ser Leu Lys Ile Pro Glu Ile Ser Ile Gln Asp Met Thr Ala Gln
 20                355             360                 365

     Val Thr Ser Pro Ser Gly Lys Thr His Glu Ala Glu Ile Val Glu Gly
                   370             375                 380

     Glu Asn His Thr Tyr Cys Ile Arg Phe Val Pro Ala Glu Met Gly Thr
                   385             390             395             400
```

```
     His Thr Val Ser Val Lys Tyr Lys Gly Gln His Val Pro Gly Ser Pro
                   405             410                 415

     Phe Gln Phe Thr Gly Pro Leu Gly Gly Gly Ala His Lys Val
                   420             425                 430

  5  Arg Ala Gly Gly Pro Gly Leu Glu Arg Ala Glu Ala Gly Val Pro Ala
                   435             440                 445

     Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly Ala Gly Gly Leu Ala Ile
                   450             455                 460

     Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Ser Phe Glu Asp Arg Lys
 10                465             470             475             480

     Asp Gly Ser Cys Gly Val Ala Tyr Val Val Gln Pro Gly Asp Tyr
                   485             490                 495

     Glu Val Ser Val Lys Phe Asn Glu Glu His Ile Pro Asp Ser Pro Phe
                   500             505                 510

 15  Val Val Pro Val Ala Ser Pro Ser Gly Asp Ala Arg Arg Leu Thr Val
                   515             520                 525

     Ser Ser Leu Gln Glu Ser Gly Leu Lys Val Asn Gln Pro Ala Ser Phe
                   530             535                 540

     Ala Val Ser Leu Asn Gly Ala Lys Gly Ala Ile Asp Ala Lys Val His
 20                545             550             555             560

     Ser Pro Ser Gly Ala Leu Glu Glu Cys Tyr Val Thr Glu Ile Asp Gln
                   565             570                 575

     Asp Lys Tyr Ala Val Arg Phe Ile Pro Arg Glu Asn Gly Val Tyr Leu
                   580             585                 590
```

Ile Asp Val Lys Phe Asn Gly Thr His Ile Pro Gly Ser Pro Phe Lys
  595   600   605

Ile Arg Val Gly Glu Pro Gly His Gly Gly Asp Pro Gly Leu Val Ser
  610   615   620

5 Ala Tyr Gly Ala Gly Leu Glu Gly Gly Val Thr Gly Asn Pro Ala Glu
  625   630   635   640

Phe Val Asn Thr Ser Asn Ala Gly Ala Leu Ser Val Thr
      645   650   655

Ile Asp Gly Pro Ser Lys Val Lys Met Asp Cys Gln Glu Cys Pro Glu
10 660   665   670

Gly Tyr Arg Val Thr Tyr Thr Pro Met Ala Pro Gly Ser Tyr Leu Ile
  675   680   685

Ser Ile Lys Tyr Gly Gly Pro Tyr His Ile Gly Gly Ser Pro Phe Lys
  690   695   700

15 Ala Lys Val Thr Gly Pro Arg Leu Val Ser Asn His Ser Leu His Glu
  705   710   715   720

Thr Ser Ser Val Phe Val Asp Ser Leu Thr Lys Ala Thr Cys Ala Pro
  725   730   735

Gln His Gly Ala Pro Gly Pro Gly Pro Ala Asp Ala Ser Lys Val Val
20 740   745   750

Ala Lys Gly Leu Gly Leu Ser Lys Ala Tyr Val Gly Gln Lys Ser Ser
  755   760   765

Phe Thr Val Asp Cys Ser Lys Ala Gly Asn Asn Met Leu Leu Val Gly
  770   775   780

Val His Gly Pro Arg Thr Pro Cys Glu Glu Ile Leu Val Lys His Val
  785   790   795   800

Gly Ser Arg Leu Tyr Ser Val Ser Tyr Leu Lys Asp Lys Gly Glu
  805   810   815

5 Tyr Thr Leu Val Val Lys Trp Gly Asp Glu His Ile Pro Gly Ser Pro
  820   825   830

Tyr Arg Val Val Pro
     835

10

<210> 61
<211> 433
<212> PRT
<213> Homo sapiens

15 <220>
<221> human alpha enolase
<222> (1)..(433)
<223> Accession No. as of 29 August 2003: P06733
<400> 61

20

Ser Ile Leu Lys Ile His Ala Arg Glu Ile Phe Asp Ser Arg Gly Asn
1   5   10   15

Pro Thr Val Glu Val Asp Leu Phe Thr Ser Lys Gly Leu Phe Arg Ala
  20   25   30

```
    Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu Ala Leu Glu Leu
                35                  40                  45

    Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly Lys Gly Val Ser Lys Ala
                50                  55                  60

5   Val Glu His Ile Asn Lys Thr Ile Ala Pro Ala Leu Val Ser Lys Lys
                65              70                  75              80

    Leu Asn Val Thr Glu Gln Glu Lys Ile Asp Lys Leu Met Ile Glu Met
                85                  90                  95

10  Asp Gly Thr Glu Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile Leu Gly
                100                 105                 110

    Val Ser Leu Ala Val Cys Lys Ala Gly Ala Val Glu Lys Gly Val Pro
                115                 120                 125

    Leu Tyr Arg His Ile Ala Asp Leu Ala Gly Asn Ser Glu Val Ile Leu
                130                 135                 140

15  Pro Val Pro Ala Phe Asn Val Ile Asn Gly Gly Ser His Ala Gly Asn
                145             150                 155             160

    Lys Leu Ala Met Gln Glu Phe Met Ile Leu Pro Val Gly Ala Ala Asn
                165                 170                 175

    Phe Arg Glu Ala Met Arg Ile Gly Ala Glu Val Tyr His Asn Leu Lys
                180                 185                 190

20  Asn Val Ile Lys Glu Lys Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp
                195                 200                 205

    Glu Gly Gly Phe Ala Pro Asn Ile Leu Glu Asn Lys Glu Gly Leu Glu
                210                 215                 220
```

```
    Leu Leu Lys Thr Ala Ile Gly Lys Ala Gly Tyr Thr Asp Lys Val Val
                225             230                 235             240

    Ile Gly Met Asp Val Ala Ala Ser Glu Phe Arg Ser Gly Lys Tyr
                245                 250                 255

5   Asp Leu Asp Phe Lys Ser Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro
                260                 265                 270

    Asp Gln Leu Ala Asp Leu Tyr Lys Ser Phe Ile Lys Asp Tyr Pro Val
                275                 280                 285

    Val Ser Ile Glu Asp Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp Gln
                290                 295                 300

10  Lys Phe Thr Ala Ser Ala Gly Ile Gln Val Val Gly Asp Asp Leu Thr
                305             310                 315             320

    Val Thr Asn Pro Lys Arg Ile Ala Lys Ala Val Asn Glu Lys Ser Cys
                325                 330                 335

15  Asn Cys Leu Leu Leu Lys Val Asn Gln Ile Gly Ser Val Thr Glu Ser
                340                 345                 350

    Leu Gln Ala Cys Lys Leu Ala Gln Ala Asn Gly Trp Gly Val Met Val
                355                 360                 365

    Ser His Arg Ser Gly Glu Thr Glu Asp Thr Phe Ile Ala Asp Leu Val
                370                 375                 380

20  Val Gly Leu Cys Thr Gly Gln Ile Lys Thr Gly Ala Pro Cys Arg Ser
                385             390                 395             400

    Glu Arg Leu Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu Glu Glu Leu
                405                 410                 415
```

```
        Gly Ser Lys Ala Lys Phe Ala Gly Arg Asn Phe Arg Asn Pro Leu Ala
                        420                 425                 430

        Lys
```

<210> 62
<211> 471
<212> PRT
<213> Homo sapiens

<220>
<221> tryptophanyl-tRNA synthetase
<222> (1)..(471)
<223> Accession No. as of 29 August 2003: P23381

<400> 62

```
        Met Pro Asn Ser Glu Pro Ala Ser Leu Leu Glu Leu Phe Asn Ser Ile
    1                   5                   10                  15

        Ala Thr Gln Gly Glu Leu Val Arg Ser Leu Lys Ala Gly Asn Ala Ser
                        20                  25                  30

        Lys Asp Glu Ile Asp Ser Ala Val Lys Met Leu Val Ser Leu Lys Met
                        35                  40                  45

        Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro
    50                  55                  60
```

```
        Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala
                        65                  70                  75                  80

        Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys
                                85                  90                  95

        Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile
    5                           100                 105                 110

        Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro
                                115                 120                 125

        His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn
    10                          130                 135                 140

        Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr
                                145                 150                 155                 160

        Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro
                                165                 170                 175

        Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val
    15                          180                 185                 190

        Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu
                                195                 200                 205

        Asp Gln Ala Tyr Ser Tyr Ala Val Glu Asn Ala Lys Asp Ile Ile Ala
    20                          210                 215                 220

        Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr
                                225                 230                 235                 240

        Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys
                                245                 250                 255
```

His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Thr Asp Ser

260   265   270

Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser

275   280   285

5   Phe Ser Asn Ser Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln

290   295   300

Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr

305   310   315   320

Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His

325   330   335

10 Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala

340   345   350

Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile

355   360   365

15 Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile

370   375   380

Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe

385   390   395   400

Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Lys Leu Glu Gln Ile

405   410   415

20 Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys

420   425   430

Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg

435   440   445

Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg

450   455   460

Lys Leu Ser Phe Asp Gln

465   470

5

<210> 63

<211> 106

<212> PRT

10 <213> Homo sapiens

<220>

<221> Ig kappa chain C regionI

<222> (1)..(106)

<223> Accession No. as of 29 August 2003: P01834

15 <400> 63

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln

1   5   10   15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr

20   25   30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser

35   40   45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr

50   55   60

```
Ala Gly Leu Leu Phe Val Gly Gly Gly Ile Gly Gly Thr Ile Leu Tyr
                50                  55                  60

Ala Lys Trp Asp Ser His Phe Arg Glu Val Lys Thr Ile Pro
                65                  70                  75                  80

Tyr Ser Asp Lys Leu Phe Glu Met Val Leu Gly Pro Ala Ala Tyr Asn
5                   85                  90                  95

Val Pro Leu Pro Lys Ser Ile Gln Ser Gly Pro Leu Lys Ile Ser
                    100                 105                 110

Ser Val Ser Glu Val Met Lys Glu Ser Lys Gln Pro Ala Ser Gln Leu
10                  115                 120                 125

Gln Lys Gln Lys Gly Asp Thr Pro Ala Ser Ala Thr Ala Pro Thr Glu
                    130                 135                 140

Ala Ala Gln Ile Ile Ser Ala Ala Gly Asp Thr Leu Ser Val Pro Ala
145                 150                 155                 160

Pro Ala Val Gln Pro Glu Glu Ser Leu Lys Thr Asp His Pro Glu Ile
15                  165                 170                 175

Gly Glu Gly Lys Pro Thr Pro Ala Leu Ser Glu Glu Ala Ser Ser Ser
                    180                 185                 190

Ser Ile Arg Glu Arg Pro Pro Glu Val Ala Ala Arg Leu Ala Gln
20                  195                 200                 205

Gln Glu Lys Gln Glu Gln Val Lys Ile Glu Ser Leu Ala Lys Ser Leu
                    210                 215                 220

Glu Asp Ala Leu Arg Gln Thr Ala Ser Val Thr Leu Gln Ala Ile Ala
225                 230                 235                 240
```

```
Tyr Ser Ser Thr Leu Thr Ser Lys Ala Asp Tyr Glu Lys
                65                  70                  75                  80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                    85                  90                  95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
5                   100                 105


<210> 64
10  <211> 758
    <212> PRT
    <213> Homo sapiens
    <220>
    <221> Mitofilin
15  <222> (1)..(758)
    <223> Accession No. as of 29 August 2003: Q16891
    <400> 64

Met Leu Arg Ala Cys Gln Leu Ser Gly Val Thr Ala Ala Gln Ser
20  1                   5                   10                  15

Cys Leu Cys Gly Lys Phe Val Leu Arg Pro Leu Arg Pro Cys Arg Arg
                    20                  25                  30

Tyr Ser Thr Ser Gly Ser Ser Gly Leu Thr Thr Gly Lys Ile Ala Gly
35                  40                  45
```

Ala Gln Asn Ala Ala Val Gln Ala Val Asn Ala His Ser Asn Ile Leu
     245   250   255

Lys Ala Ala Met Asp Asn Ser Glu Ile Ala Gly Gly Lys Lys Ser Ala
     260   265   270

5 Gln Trp Arg Thr Val Glu Gly Ala Leu Lys Glu Arg Arg Lys Ala Val
     275   280   285

Asp Glu Ala Ala Asp Ala Leu Leu Lys Ala Lys Glu Glu Leu Glu Lys
     290   295   300

Met Lys Ser Val Ile Glu Asn Ala Lys Lys Lys Glu Val Ala Gly Ala
10 305   310   315   320

Lys Pro His Ile Thr Ala Ala Glu Gly Lys Leu His Asn Met Ile Val
     325   330   335

Asp Leu Asp Asn Val Val Lys Val Gln Ala Ala Gln Ser Glu Ala
     340   345   350

15 Lys Val Val Ser Gln Tyr His Glu Leu Val Val Gln Ala Arg Asp Asp
     355   360   365

Phe Lys Arg Glu Leu Asp Ser Ile Thr Pro Glu Val Leu Pro Gly Trp
     370   375   380

Lys Gly Met Ser Val Ser Asp Leu Ala Asp Lys Leu Ser Thr Asp Asp
20 385   390   395   400

Leu Asn Ser Leu Ile Ala His Ala His Arg Arg Ile Asp Gln Leu Asn
     405   410   415

Arg Glu Leu Ala Glu Gln Lys Ala Thr Glu Lys Gln His Ile Thr Leu
     420   425   430

Ala Leu Glu Lys Gln Leu Glu Lys Glu Glu Arg Ala Phe Asp Ser Ala
     435   440   445

Val Ala Lys Ala Leu Glu His Arg Ser Glu Ile Gln Ala Glu Gln
     450   455   460

5 Asp Arg Lys Ile Glu Glu Arg Asp Ala Met Glu Asn Glu Met Arg
     465   470   475   480

Thr Gln Leu Arg Arg Gln Ala Ala Ala His Thr Asp His Leu Arg Asp
     485   490   495

Val Leu Arg Val Gln Gln Gln Leu Gln Leu Lys Ser Glu Phe Glu Gln Asn
10 500   505   510

Leu Ser Glu Lys Leu Ser Glu Gln Glu Gln Phe Arg Arg Leu Ser
     515   520   525

Gln Glu Gln Val Asp Asp Phe Thr Leu Asp Ile Asn Thr Ala Tyr Ala
     530   535   540

15 Arg Leu Arg Gly Ile Glu Gln Ala Val Gln Ser His Ala Val Ala Glu
     545   550   555   560

Glu Glu Ala Arg Lys Ala His Gln Leu Trp Leu Ser Val Glu Ala Leu
     565   570   575

Lys Tyr Ser Met Lys Thr Ser Ser Ala Glu Thr Pro Thr Ile Pro Leu
20 580   585   590

Gly Ser Ala Val Glu Ala Ile Lys Ala Asn Cys Ser Asp Asn Glu Phe
     595   600   605

Thr Gln Ala Leu Thr Ala Ala Ile Pro Pro Glu Ser Leu Thr Arg Gly
     610   615   620

```
<220>

<221>  Ribisome-binding protein 1

<222>  (1)..(1410)

<223>  Accession No. as of 29 August 2003: O75300

<400>  65


Met Asp Ile Tyr Asp Thr Gln Thr Leu Gly Val Val Val Phe Gly Gly
1                   5                   10                  15

Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
            20                  25                  30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
        35                  40                  45

Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Glu Lys
    50                  55                  60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65                  70                  75                  80

Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu
            85                  90                  95

Arg Glu Pro Val Arg Ala Pro Ala Ala Val Ala Val Ala Pro Thr Pro Val
            100                 105                 110

Gln Pro Pro Ile Ile Val Ala Pro Val Ala Thr Val Pro Ala Met Pro
            115                 120                 125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Glu Lys
        130                 135                 140
```

```
Val Tyr Ser Glu Glu Thr Leu Arg Arg Ala Phe Tyr Ala Val Gln Lys
625                 630                 635                 640

Leu Ala Arg Arg Val Ala Met Ile Asp Glu Thr Arg Asn Ser Leu Tyr
            645                 650                 655

Gln Tyr Phe Leu Ser Tyr Leu Gln Ser Leu Leu Phe Pro Pro Gln
5               660                 665                 670

Gln Leu Lys Pro Pro Glu Leu Cys Pro Glu Asp Ile Asn Thr Phe
            675                 680                 685

Lys Leu Leu Ser Tyr Ala Ser Tyr Cys Ile Glu His Gly Asp Leu Glu
10          690                 695                 700

Leu Ala Ala Lys Phe-Val Asn Gln Leu Lys Gly Glu Ser Arg Arg Val
            705                 710                 715                 720

Ala Gln Asp Trp Leu Lys Glu Ala Arg Met Thr Leu Glu Thr Lys Gln
            725                 730                 735

Ile Val Glu Ile Leu Thr Ala Tyr Ala Ser Ala Val Gly Ile Gly Thr
15          740                 745                 750

Thr Gln Val Gln Pro Glu
            755


<210>  65

<211>  1410

<212>  PRT

<213>  Homo sapiens
```

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
                        340   345   350

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
                355   360   365

Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ser Glu Gly
5   370   375   380

Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys
                385   390   395   400

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
10   405   410   415

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
                420   425   430

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
435   440   445

Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
15   450   455   460

Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys Lys
465   470   475   480

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Gln
20   485   490   495

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Gln Lys Gly
                500   505   510

Glu Gly Ala Gln Asn Gln Gly Lys Lys Thr Glu Gly Ala Gln Gly Lys
515   520   525

Lys Val Ala Lys Glu Val Pro Ala Val Ser Ser Val Val Asn Ser Ile
                145   150   155   160

Gln Val Leu Thr Ser Lys Ala Ala Ile Glu Leu Thr Ala Pro Lys Glu
                165   170   175

Val Pro Met Val Val Pro Val Gly Ala Lys Gly Asn Thr Pro
5   180   185   190

Ala Thr Gly Thr Gln Gly Lys Lys Ala Glu Gly Thr Gln Asn Gln
                195   200   205

Ser Lys Ala Glu Gly Ala Pro Asn Gln Gly Arg Lys Ala Glu Gly
10   210   215   220

Thr Pro Asn Gln Gly Lys Lys Thr Glu Gly Thr Pro Asn Gln Gly Lys
225   230   235   240

Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro
                245   250   255

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val
15   260   265   270

Asp Thr Thr Pro Asn Gln Gly Lys Lys Val Glu Gly Ala Pro Thr Gln
                275   280   285

Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val Glu Gly
20   290   295   300

Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys
                305   310   315   320

Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
                325   330   335

Lys Ala Glu Ser Pro Asn Gln Gly Lys Gly Glu Gly Ala Pro
                    530   535   540

Ile Gln Gly Lys Lys Ala Asp Ser Val Ala Asn Gln Gly Thr Lys Val
      545   550   555   560

5   Glu Gly Ile Thr Asn Gln Gly Lys Lys Ala Glu Gly Ser Pro Ser Glu
                    565   570   575

Gly Lys Lys Ala Glu Gly Ser Pro Asn Gln Gly Lys Lys Ala Asp Ala
                    580   585   590

10 Ala Ala Asn Gln Gly Lys Lys Thr Glu Ser Ala Ser Val Gln Gly Arg
                    595   600   605

Asn Thr Asp Val Ala Gln Ser Pro Glu Ala Pro Lys Gln Glu Ala Pro
                    610   615   620

Ala Lys Lys Ser Gly Ser Lys Lys Gly Glu Pro Gly Pro Pro
                    625   630   635   640

15 Asp Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val Ser Thr
                    645   650   655

Val Gly Ser Met Val Phe Asn Glu Gly Glu Gln Arg Leu Ile Glu
                    660   665   670

Ile Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His Lys Ala
                    675   680   685

20 Thr Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu
                    690   695   700

Lys Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys
                    705   710   715   720

Ser Lys Leu Arg Glu Leu Asn Lys Glu Lys Glu Met Ala Ala Lys Ala Lys
                    725   730   735

Ala Ala Ala Gly Glu Glu Lys Val Lys Gln Leu Val Ala Arg Glu
                    740   745   750

5   Gln Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu
                    755   760   765

His Val Lys Glu Val Gln Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln
                    770   775   780

10 785 Glu Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln
                                        790   795   800

Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val
                    805   810   815

Glu Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser
                    820   825   830

15 Lys Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Val Arg Gln Asp
                    835   840   845

Glu Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Phe Glu Lys
                    850   855   860

Gln Val Leu Gln Leu Gln Ala Ser His Arg Glu Ser Glu Glu Ala Leu
                    865   870   875   880

20 Gln Lys Arg Leu Asp Glu Val Ser Arg Glu Leu Cys His Thr Gln Ser
                    885   890   895

Ser His Ala Ser Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln
                    900   905   910

Gln Gln Met Ala Glu His Ser Lys Leu Gln Ser Ser Glu Ala Glu
915   920   925

Val Arg Ser Lys Cys Glu Glu Leu Ser Gly Leu His Gly Gln Leu Gln
930   935   940

5 Glu Ala Arg Ala Glu Asn Ser Gln Leu Thr Glu Ile Arg Ser Ile
945   950   955   960

Glu Ala Leu Leu Glu Ala Gly Gln Ala Arg Asp Ala Gln Asp Val Gln
965   970   975

Ala Ser Gln Ala Glu Ala Asp Gln Gln Thr Arg Leu Lys Glu Leu
10   980   985   990

Glu Ser Gln Val Ser Gly Leu Glu Lys Glu Ala Ile Glu Leu Arg Glu
995   1000   1005

Ala Val Glu Gln Gln Lys Val Lys Asn Asn Asp Leu Arg Arg Glu Lys
1010   1015   1020

15 Asn Trp Lys Ala Met Glu Ala Leu Ala Thr Ala Glu Gln Ala Cys
1025   1030   1035

Lys Glu Leu Leu Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu
1040   1045   1050

Lys Gln Leu Cys Leu Ile Glu Ala Gln Thr Met Glu Ala Leu Leu
20   1055   1060   1065

Ala Leu Leu Pro Glu Leu Ser Val Leu Ala Gln Gln Asn Tyr Thr
1070   1075   1080

Glu Trp Leu Gln Asp Leu Lys Glu Lys Gly Pro Thr Leu Leu Lys
1085   1090   1095

His Pro Pro Ala Pro Ala Glu Pro Ser Ser Asp Leu Ala Ser Lys
1100   1105   1110

Leu Arg Glu Ala Glu Glu Thr Gln Ser Thr Leu Gln Ala Glu Cys
1115   1120   1125

5 Asp Gln Tyr Arg Ser Ile Leu Ala Glu Thr Glu Gly Met Leu Arg
1130   1135   1140

Asp Leu Gln Lys Ser Val Glu Glu Glu Glu Gln Val Trp Arg Ala
1145   1150   1155

Lys Val Gly Ala Ala Glu Glu Glu Leu Gln Lys Ser Arg Val Thr
10   1160   1165   1170

Val Lys His Leu Glu Glu Ile Val Glu Lys Leu Lys Gly Glu Leu
1175   1180   1185

Glu Ser Ser Asp Gln Val Arg Glu His Thr Ser His Leu Glu Ala
1190   1195   1200

15 Glu Leu Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln Asn
1205   1210   1215

Tyr Ala Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Glu Ser
1220   1225   1230

Gln Ser Gln Leu Asp Ala Ala Lys Ser Glu Ala Gln Lys Gln Ser
20   1235   1240   1245

Asp Glu Leu Ala Leu Val Arg Gln Gln Leu Ser Glu Met Lys Ser
1250   1255   1260

His Val Glu Asp Gly Asp Ile Ala Gly Ala Pro Ala Ser Ser Pro
1265   1270   1275

<220>

<221> Fibrinogen gamma chain precursor

<222> (1)..(453)

<223> Accession No. as of 29 August 2003: P02679

5   <400> 66

Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala
1   5   10   15

Leu Leu Phe Leu Ser Ser Thr Cys Val Ala Tyr Val Ala Thr Arg Asp
10   20   25   30

Asn Cys Cys Ile Leu Asp Glu Arg Phe Gly Ser Tyr Cys Pro Thr Thr
            35   40   45

Cys Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys
    50   55   60

Asp Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr
15 65   70   75   80

Ser Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro
                85   90   95

Asp Glu Ser Ser Lys Pro Asn Met Ile Asp Ala Ala Thr Leu Lys Ser
20   100   105   110

Arg Lys Met Leu Glu Glu Ile Met Lys Tyr Glu Ala Ser Ile Leu Thr
            115   120   125

His Asp Ser Ser Ile Arg Tyr Leu Gln Glu Ile Tyr Asn Ser Asn Asn
        130   135   140

Glu Ala Pro Pro Ala Glu Gln Asp Pro Val Gln Leu Lys Thr Gln
         1280   1285   1290

Leu Glu Trp Thr Glu Ala Ile Leu Glu Asp Glu Gln Thr Gln Arg
         1295   1300   1305

5   Gln Lys Leu Thr Ala Glu Phe Glu Glu Ala Gln Thr Ser Ala Cys
             1310   1315   1320

Arg Leu Gln Glu Glu Leu Glu Lys Leu Arg Thr Ala Gly Pro Leu
         1325   1330   1335

Glu Ser Ser Glu Thr Glu Glu Ala Ser Gln Leu Lys Glu Arg Leu
10   1340   1345   1350

Glu Lys Glu Lys Lys Leu Thr Ser Asp Leu Gly Arg Ala Ala Thr
         1355   1360   1365

Arg Leu Gln Glu Leu Leu Lys Thr Thr Gln Glu Gln Leu Ala Arg
         1370   1375   1380

15 Glu Lys Asp Thr Val Lys Lys Leu Gln Glu Gln Leu Glu Lys Ala
             1385   1390   1395

Glu Asp Gly Ser Ser Ser Lys Glu Gly Thr Ser Val
         1400   1405   1410

20

<210> 66

<211> 453

<212> PRT

<213> Homo sapiens

```
     Gln Lys Ile Val Asn Leu Lys Glu Lys Val Ala Gln Leu Glu Ala Gln
     145                 150                 155                 160

     Cys Gln Glu Pro Cys Lys Asp Thr Val Gln Ile His Asp Ile Thr Gly
                     165                 170                 175

     Lys Asp Cys Gln Asp Ile Ala Asn Lys Gly Ala Lys Gln Ser Gly Leu
   5                 180                 185                 190

     Tyr Phe Ile Lys Pro Leu Lys Ala Asn Gln Gln Phe Leu Val Tyr Cys
                     195                 200                 205

     Glu Ile Asp Gly Ser Gly Asn Gly Trp Thr Val Phe Gln Lys Arg Leu
  10                 210                 215                 220

     Asp Gly Ser Val Asp Phe Lys Lys Asn Trp Ile Gln Tyr Lys Glu Gly
                     225                 230                 235             240

     Phe Gly His Leu Ser Pro Thr Gly Thr Glu Phe Trp Leu Gly Asn
                     245                 250                 255

     Glu Lys Ile His Leu Ile Ser Thr Gln Ser Ala Ile Pro Tyr Ala Leu
  15                 260                 265                 270

     Arg Val Glu Leu Glu Asp Trp Asn Gly Arg Thr Ser Thr Ala Asp Tyr
                     275                 280                 285

     Ala Met Phe Lys Val Gly Pro Glu Ala Asp Lys Tyr Arg Leu Thr Tyr
  20                 290                 295                 300

     Ala Tyr Phe Ala Gly Gly Asp Ala Gly Asp Ala Phe Asp Gly Phe Asp
                     305                 310                 315             320

     Phe Gly Asp Asp Pro Ser Asp Lys Phe Phe Thr Ser His Asn Gly Met
                     325                 330                 335
```

```
     Gln Phe Ser Thr Trp Asp Asn Asp Asn Asp Lys Phe Glu Gly Asn Cys
                     340                 345                 350

     Ala Glu Gln Asp Gly Ser Gly Trp Trp Met Asn Lys Cys His Ala Gly
                     355                 360                 365

     His Leu Asn Gly Val Tyr Tyr Gln Gly Gly Thr Tyr Ser Lys Ala Ser
   5                 370                 375                 380

     Thr Pro Asn Gly Tyr Asp Asn Gly Ile Ile Trp Ala Thr Trp Lys Thr
                     385                 390                 395             400

     Arg Trp Tyr Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro Phe Asn
  10                 405                 410                 415

     Arg Leu Thr Ile Gly Glu Gly Gln His His Leu Gly Gly Ala Lys
                     420                 425                 430

     Gln Val Arg Pro Glu His Pro Ala Glu Thr Glu Tyr Asp Ser Leu Tyr
                     435                 440                 445

     Pro Glu Asp Asp Leu
  15                 450


     <210> 67

  20 <211> 622

     <212> PRT

     <213> Homo sapiens

     <220>

     <221> Prothrombin precursor
```

<222> (1)..(622)

<223> Accession No. as of 29 August 2003: P00734

<400> 67

```
5   Met Ala His Val Arg Gly Leu Gln Leu Pro Gly Cys Leu Ala Leu Ala
    1               5                   10                  15
    Ala Leu Cys Ser Leu Val His Ser Gln His Val Phe Leu Ala Pro Gln
                20                  25                  30
    Gln Ala Arg Ser Leu Gln Arg Val Arg Arg Ala Asn Thr Phe Leu
10          35                  40                  45
    Glu Glu Arg Lys Gly Asn Leu Glu Arg Glu Cys Val Glu Glu Thr
            50                  55                  60
    Cys Ser Tyr Glu Glu Ala Phe Glu Ala Leu Glu Ser Ser Thr Ala Thr
    65                  70                  75                  80
15  Asp Val Phe Trp Ala Lys Tyr Thr Ala Cys Glu Thr Ala Arg Thr Pro
                    85                  90                  95
    Arg Asp Lys Leu Ala Ala Cys Leu Glu Gly Asn Cys Ala Glu Gly Leu
                    100                 105                 110
    Gly Thr Asn Tyr Arg Gly His Val Asn Ile Thr Arg Ser Gly Ile Glu
            115                 120                 125
    Cys Gln Leu Trp Arg Ser Arg Tyr Pro His Lys Pro Glu Ile Asn Ser
20          130                 135                 140
    Thr Thr His Pro Gly Ala Asp Leu Gln Glu Asn Phe Cys Arg Asn Pro
    145                 150                 155                 160
```

```
    Asp Ser Ser Thr Gly Pro Trp Cys Tyr Thr Thr Asp Pro Thr Val
                    165                 170                 175
    Arg Arg Gln Glu Cys Ser Ile Pro Val Cys Gly Gln Asp Gln Val Thr
                    180                 185                 190
5   Val Ala Met Thr Pro Arg Ser Glu Gly Ser Ser Val Asn Leu Ser Pro
                    195                 200                 205
    Pro Leu Glu Gln Cys Val Pro Asp Arg Gly Gln Gln Tyr Gln Gly Arg
            210                 215                 220
    Leu Ala Val Thr Thr His Gly Leu Pro Cys Leu Ala Trp Ala Ser Ala
10  225                 230                 235                 240
    Gln Ala Lys Ala Leu Ser Lys His Gln Asp Phe Asn Ser Ala Val Gln
                    245                 250                 255
    Leu Val Glu Asn Phe Cys Arg Asn Pro Asp Gly Asp Glu Glu Gly Val
            260                 265                 270
15  Trp Cys Tyr Val Ala Gly Lys Pro Gly Asp Phe Gly Tyr Cys Asp Leu
            275                 280                 285
    Asn Tyr Cys Glu Glu Ala Val Glu Glu Glu Thr Gly Asp Gly Leu Asp
            290                 295                 300
    Glu Asp Ser Asp Arg Ala Ile Glu Gly Arg Thr Ala Thr Ser Glu Tyr
20  305                 310                 315                 320
    Gln Thr Phe Phe Asn Pro Arg Thr Phe Gly Ser Gly Glu Ala Asp Cys
            325                 330                 335
    Gly Leu Arg Pro Leu Phe Glu Lys Lys Ser Leu Glu Asp Lys Thr Glu
            340                 345                 350
```

Arg Glu Leu Leu Glu Ser Tyr Ile Asp Gly Arg Ile Val Glu Gly Ser
    355   360   365

Asp Ala Glu Ile Gly Met Ser Pro Trp Gln Val Met Leu Phe Arg Lys
  370   375   380

5 Ser Pro Gln Glu Leu Leu Cys Gly Ala Ser Leu Ile Ser Asp Arg Trp
  385   390   395   400

Val Leu Thr Ala Ala His Cys Leu Leu Tyr Pro Pro Trp Asp Lys Asn
    405   410   415

Phe Thr Glu Asn Asp Leu Leu Val Arg Ile Gly Lys His Ser Arg Thr
10 420   425   430

Arg Tyr Glu Arg Asn Ile Glu Lys Ile Ser Met Leu Glu Lys Ile Tyr
  435   440   445

Ile His Pro Arg Tyr Asn Trp Arg Glu Asn Leu Asp Arg Asp Ile Ala
  450   455   460

15 Leu Met Lys Leu Lys Lys Pro Val Ala Phe Ser Asp Tyr Ile His Pro
  465   470   475   480

Val Cys Leu Pro Asp Arg Glu Thr Ala Ala Ser Leu Leu Gln Ala Gly
    485   490   495

Tyr Lys Gly Arg Val Thr Gly Trp Gly Asn Leu Lys Glu Thr Trp Thr
20 500   505   510

Ala Asn Val Gly Lys Gly Gln Pro Ser Val Leu Gln Val Val Asn Leu
  515   520   525

Pro Ile Val Glu Arg Pro Val Cys Lys Asp Ser Thr Arg Ile Arg Ile
  530   535   540

Thr Asp Asn Met Phe Cys Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg
  545   550   555   560

Gly Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Phe Val Met Lys Ser
    565   570   575

5 Pro Phe Asn Asn Arg Trp Tyr Gln Met Gly Ile Val Ser Trp Gly Glu
    580   585   590

Gly Cys Asp Arg Asp Gly Lys Tyr Gly Phe Tyr Thr His Val Phe Arg
    595   600   605

Leu Lys Lys Trp Ile Gln Lys Val Ile Asp Gln Phe Gly Glu
10 610   615   620

<210> 68
<211> 530
15 <212> PRT
<213> Homo sapiens
<220>
<221> Pyruvate kinase
<222> (1)..(530)
20 <223> Accession No. as of 29 August 2003: P14618

<400> 68

Ser Lys Pro His Ser Glu Ala Gly Thr Ala Phe Ile Gln Thr Gln Gln
1   5   10   15

Leu His Ala Ala Met Ala Asp Thr Phe Leu Glu His Met Cys Arg Leu
20 25 30

Asp Ile Asp Ser Pro Ile Thr Ala Arg Asn Thr Gly Ile Ile Cys
35 40 45

5 Thr Ile Gly Pro Ala Ser Arg Ser Val Glu Thr Leu Lys Glu Met Ile
50 55 60

Lys Ser Gly Met Asn Val Ala Arg Leu Asn Phe Ser His Gly Thr His
65 70 75 80

Glu Tyr His Ala Glu Thr Ile Lys Asn Val Arg Thr Ala Thr Glu Ser
85 90 95

10 Phe Ala Ser Asp Pro Ile Leu Tyr Arg Pro Val Ala Val Ala Leu Asp
100 105 110

Thr Lys Gly Pro Glu Ile Arg Thr Gly Leu Ile Lys Gly Ser Gly Thr
115 120 125

15 Ala Glu Val Glu Leu Lys Lys Gly Ala Thr Leu Lys Ile Thr Leu Asp
130 135 140

Asn Ala Tyr Met Glu Lys Cys Asp Glu Asn Ile Leu Trp Leu Asp Tyr
145 150 155 160

Lys Asn Ile Cys Lys Val Val Glu Val Gly Ser Lys Ile Tyr Val Asp
165 170 175

20 Asp Gly Leu Ile Ser Leu Gln Val Lys Gln Lys Gly Ala Asp Phe Leu
180 185 190

Val Thr Glu Val Glu Asn Gly Gly Ser Leu Gly Ser Lys Lys Gly Val
195 200 205

Asn Leu Pro Gly Ala Ala Val Asp Leu Pro Ala Val Ser Glu Lys Asp
210 215 220

Ile Gln Asp Leu Lys Phe Gly Val Glu Gln Asp Val Asp Met Val Phe
225 230 235 240

5 Ala Ser Phe Ile Arg Lys Ala Ser Asp Val His Glu Val Arg Lys Val
245 250 255

Leu Gly Glu Lys Gly Lys Asn Ile Lys Ile Ile Ser Lys Ile Glu Asn
260 265 270

His Glu Gly Val Arg Arg Phe Asp Glu Ile Leu Glu Ala Ser Asp Gly
275 280 285

10 Ile Met Val Ala Arg Gly Asp Leu Gly Ile Glu Ile Pro Ala Glu Lys
290 295 300

Val Phe Leu Ala Gln Lys Met Met Ile Gly Arg Cys Asn Arg Ala Gly
305 310 315 320

15 Lys Pro Val Ile Cys Ala Thr Gln Met Leu Glu Ser Met Ile Lys Lys
325 330 335

Pro Arg Pro Thr Arg Ala Glu Gly Ser Asp Val Ala Asn Ala Val Leu
340 345 350

Asp Gly Ala Asp Cys Ile Met Leu Ser Gly Glu Thr Ala Lys Gly Asp
355 360 365

20 Tyr Pro Leu Glu Ala Val Arg Met Gln His Leu Ile Ala Arg Glu Ala
370 375 380

Glu Ala Ala Ile Tyr His Leu Gln Leu Phe Glu Glu Leu Arg Arg Leu
385 390 395 400

```
Ala Pro Ile Thr Ser Asp Pro Thr Glu Ala Thr Ala Val Gly Ala Val
                    405                 410                 415

Glu Ala Ser Phe Lys Cys Cys Ser Gly Ala Ile Ile Val Leu Thr Lys
                    420                 425                 430

5   Ser Gly Arg Ser Ala His Gln Val Ala Arg Tyr Arg Pro Arg Ala Pro
                435                 440                 445

Ile Ile Ala Val Thr Arg Asn Pro Gln Thr Ala Arg Gln Ala His Leu
                    450                 455                 460

Tyr Arg Gly Ile Phe Pro Val Leu Cys Lys Asp Pro Val Gln Glu Ala
10  465                 470                 475                 480

Trp Ala Glu Asp Val Asp Leu Arg Val Asn Phe Ala Met Asn Val Gly
                    485                 490                 495

Lys Ala Arg Gly Phe Phe Lys Gly Asp Val Val Ile Val Leu Thr
                    500                 505                 510

15  Gly Trp Arg Pro Gly Ser Gly Phe Thr Asn Thr Met Arg Val Val Pro
                515                 520                 525

Val Pro
530
```

<210> 69
<211> 328
<212> PRT
<213> Homo sapiens

<220>
<221> Reticulocalbin 3 precursor

<222> (1)..(328)

<223> Accession No. as of 29 August 2003: Q96D15

5 <400> 69

```
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His
1                   5                   10                  15

Gly Ala Gln Gly Lys Pro Ser Asp Ala Gly Pro His Gly Gln Gly
10              20                  25                  30

Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Ala
                35                  40                  45

His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val
50                  55                  60

15  Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Ser Gln Ala Arg Leu
65                  70                  75                  80

Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
                    85                  90                  95

Val Ser Leu Ala Glu Leu Arg Ala Ala Trp Ile Ala His Thr Gln Gln Arg
20              100                 105                 110

His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp
                115                 120                 125

Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly
                130                 135                 140
```

```
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
145                 150                 155                 160
Tyr Lys Met Leu Ala Arg Asp Glu Arg Phe Arg Val Ala Asp
            165                 170                 175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
5           180                 185                 190
His Pro Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
            195                 200                 205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
10          210                 215                 220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Pro Ala
            225                 230                 235                 240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
            245                 250                 255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
15          260                 265                 270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
            275                 280                 285
Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
20          290                 295                 300
Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
            305                 310                 315                 320
Leu Thr Arg His His Asp Glu Leu
            325
```

```
<210> 70
<211> 469
<212> PRT
<213> Homo sapiens
<220>
<221> Desmin
<222> (1)..(469)
<223> Accession No. as of 29 August 2003: P17661
<400> 70

Ser Gln Ala Tyr Ser Ser Ser Gln Arg Val Ser Ser Tyr Arg Arg Thr
1               5                   10                  15
Phe Gly Gly Ala Pro Gly Phe Pro Leu Ser Ser Pro
            20                  25                  30
Val Phe Pro Arg Ala Gly Phe Gly Ser Lys Gly Ser Ser Ser Ser Val
35                  40                  45
Thr Ser Arg Val Tyr Gln Val Ser Arg Thr Ser Gly Gly Ala Gly Gly
50                  55                  60
Leu Gly Ser Leu Arg Ala Ser Arg Leu Gly Thr Thr Arg Thr Pro Ser
65                  70                  75                  80
Ser Tyr Gly Ala Gly Glu Leu Leu Asp Phe Ser Leu Ala Asp Ala Val
            85                  90                  95
```

```
     Asn Gln Glu Phe Leu Thr Thr Arg Thr Asn Glu Lys Val Glu Leu Gln
                     100                 105                 110

     Glu Leu Asn Asp Arg Phe Ala Asn Tyr Ile Glu Lys Val Arg Phe Leu
                     115                 120                 125

5    Glu Gln Gln Asn Ala Ala Leu Ala Ala Glu Val Asn Arg Leu Lys Gly
                     130                 135                 140

     Arg Glu Pro Thr Arg Val Ala Glu Leu Tyr Glu Glu Glu Leu Arg Glu
                     145                 150                 155         160

     Leu Arg Arg Gln Val Glu Val Leu Thr Asn Gln Arg Ala Arg Val Asp
10                   165                 170                 175

     Val Glu Arg Asp Asn Leu Asp Asp Gln Leu Arg Leu Lys Ala Lys
                     180                 185                 190

     Leu Gln Glu Ile Gln Leu Lys Glu Glu Ala Glu Asn Asn Leu Ala
                     195                 200                 205

15   Ala Phe Arg Ala Asp Val Asp Ala Ala Thr Leu Ala Arg Ile Asp Leu
                     210                 215                 220

     Glu Arg Arg Ile Glu Ser Leu Asn Glu Glu Ile Ala Phe Leu Lys Lys
                     225                 230                 235         240

     Val His Glu Glu Ile Arg Glu Leu Gln Ala Gln Leu Gln Glu Gln
20                   245                 250                 255

     Gln Val Gln Val Glu Met Asp Met Ser Lys Pro Asp Leu Thr Ala Ala
                     260                 265                 270

     Leu Arg Asp Ile Arg Ala Gln Tyr Glu Thr Ile Ala Ala Lys Asn Ile
                     275                 280                 285
```

```
     Ser Glu Ala Glu Glu Trp Tyr Lys Ser Lys Val Ser Asp Leu Thr Gln
                     290                 295                 300

     Ala Ala Asn Lys Asn Asn Asp Ala Leu Arg Gln Ala Lys Gln Glu Met
                     305                 310                 315         320

5    Met Glu Tyr Arg His Gln Ile Gln Ser Tyr Thr Cys Glu Ile Asp Ala
                     325                 330                 335

     Leu Lys Gly Thr Asn Asp Ser Leu Met Arg Gln Met Arg Glu Leu Glu
                     340                 345                 350

     Asp Arg Phe Ala Ser Glu Ala Ser Gly Tyr Gln Asp Asn Ile Ala Arg
10                   355                 360                 365

     Leu Glu Glu Ile Arg His Leu Lys Asp Glu Met Ala Arg His Leu
                     370                 375                 380

     Arg Glu Tyr Gln Asp Leu Leu Asn Val Lys Met Ala Leu Asp Val Glu
                     385                 390                 395         400

15   Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Ser Arg Ile Asn
                     405                 410                 415

     Leu Pro Ile Gln Thr Tyr Ser Ala Leu Asn Phe Arg Glu Thr Ser Pro
                     420                 425                 430

     Glu Gln Arg Gly Ser Glu Val His Thr Lys Thr Val Met Ile Lys
20                   435                 440                 445

     Thr Ile Glu Thr Arg Asp Gly Glu Val Val Ser Glu Ala Thr Gln Gln
                     450                 455                 460

     Gln His Glu Val Leu
                     465
```

<210> 71
<211> 417
<212> PRT
<213> Homo sapiens
<220>
<221> Carboxypeptidase B precursor
<222> (1)..(417)
<223> Accession No. as of 29 August 2003: P15086
<400> 71

```
Met Leu Ala Leu Leu Val Leu Val Thr Val Ala Leu Ala Ser Ala His
1               5                   10                  15
His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn Val
            20                  25                  30
Glu Asp Glu Asn His Ile Asn Ile Arg Glu Ile Ala Ser Thr Thr
        35                  40                  45
Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro His
    50                  55                  60
Ser Thr Val Asp Phe Arg Val Lys Ala Ala Glu Asp Thr Val Thr Val Glu
65                  70                  75                  80
Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser Asn
        85                  90                  95
```

```
Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Ala Thr
                100                 105                 110
Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr Ile Glu Ala Trp
                115                 120                 125
Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile Ser Arg Ser Val
            130                 135                 140
Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu Leu Lys Val Gly
        145                 150                 155                 160
Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp Cys Gly Phe His
        165                 170                 175
Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp Phe Val Arg Glu
        180                 185                 190
Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr Glu Leu Leu Asp
        195                 200                 205
Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile Asp Gly Tyr Ile
        210                 215                 220
Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr Arg Ser Thr His
        225                 230                 235                 240
Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg Asn Phe Asp Ala
        245                 250                 255
Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys Asp Glu Thr Tyr
        260                 265                 270
Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys Ala Leu Ala Asp
        275                 280                 285
```

```
Phe Ile Arg Asn Lys Ser Leu Ser Ser Ile Lys Ala Tyr Leu Thr Ile His
            290                 295                 300

Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr Ala Tyr Lys Leu
            305                 310                 315             320

Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys Ala Thr Val Lys
5           325                 330                 335

Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr Gly Pro Gly Ala
            340                 345                 350

Thr Ile Tyr Pro Ala Ala Gly Gly Ser Asp Asp Trp Ala Tyr Asp
10          355                 360                 365

Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr Gly Arg
            370                 375                 380

Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala Thr Cys Glu Glu
15          385                 390                 395             400

Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val Leu Glu His Leu
            405                 410                 415

Tyr
```

<210> 72
<211> 419
<212> PRT
<213> Homo sapiens

<220>

<221> Carboxypeptidase A1 precursor

<222> (1)..(419)

<223> Accession No. as of 29 August 2003: P15085

<400> 72

```
Met Arg Gly Leu Leu Val Leu Ser Val Leu Leu Gly Ala Val Phe Gly
1               5                   10                  15

Lys Glu Asp Phe Val Gly His Gln Val Leu Arg Ile Ser Val Ala Asp
10              20                  25                  30

Glu Ala Gln Val Gln Lys Val Lys Glu Leu Glu Asp Leu Glu His Leu
                35                  40                  45

Gln Leu Asp Phe Trp Arg Gly Pro Ala His Pro Gly Ser Pro Ile Asp
                50                  55                  60

Val Arg Val Pro Phe Pro Ser Ile Gln Ala Val Lys Ile Phe Leu Glu
15              65                  70                  75          80

Ser His Gly Ile Ser Tyr Glu Thr Met Ile Glu Asp Val Gln Ser Leu
                85                  90                  95

Leu Asp Glu Glu Gln Glu Gln Met Phe Ala Phe Arg Ser Arg Ala Arg
20              100                 105                 110

Ser Thr Asp Thr Phe Asn Tyr Ala Thr Tyr His Thr Leu Glu Glu Ile
                115                 120                 125

Tyr Asp Phe Leu Asp Leu Leu Val Ala Glu Asn Pro His Leu Val Ser
                130                 135                 140
```

Lys Ile Gln Ile Gly Asn Thr Tyr Glu Gly Arg Pro Ile Tyr Val Leu
145   150   155   160

Lys Phe Ser Thr Gly Gly Ser Lys Arg Pro Ala Ile Trp Ile Asp Thr
                 165   170   175

Gly Ile His Ser Arg Glu Trp Val Thr Gln Ala Ser Gly Val Trp Phe
5   180   185   190

Ala Lys Lys Ile Thr Gln Asp Tyr Gly Gln Asp Ala Ala Phe Thr Ala
                     195   200   205

Ile Leu Asp Thr Leu Asp Ile Phe Leu Glu Ile Val Thr Asn Pro Asp
10   210   215   220

Gly Phe Ala Phe Thr His Ser Thr Asn Arg Met Trp Arg Lys Thr Arg
                     225   230   235   240

Ser His Thr Ala Gly Ser Leu Cys Ile Gly Val Asp Pro Asn Arg Asn
                     245   250   255

Trp Asp Ala Gly Phe Gly Leu Ser Gly Ala Ser Ser Asn Pro Cys Ser
15   260   265   270

Glu Thr Tyr His Gly Lys Phe Ala Asn Ser Glu Val Glu Val Lys Ser
                     275   280   285

Ile Val Asp Phe Val Lys Asp His Gly Asn Ile Lys Ala Phe Ile Ser
20   290   295   300

Ile His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr Lys Thr
                     305   310   315   320

Glu Pro Val Pro Asp Gln Asp Glu Leu Asp Gln Leu Ser Lys Ala Ala
                     325   330   335

Val Thr Ala Leu Ala Ser Leu Tyr Gly Thr Lys Phe Asn Tyr Gly Ser
                     340   345   350

Ile Ile Lys Ala Ile Tyr Gln Ala Ser Gly Ser Thr Ile Asp Trp Thr
                     355   360   365

Tyr Ser Gln Gly Ile Lys Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr
5   370   375   380

Gly Arg Tyr Gly Phe Leu Leu Pro Ala Ser Gln Ile Ile Pro Thr Ala
                     385   390   395   400

Lys Glu Thr Trp Leu Ala Leu Leu Thr Ile Met Glu His Thr Leu Asn
10   405   410   415

His Pro Tyr

15 <210> 73
    <211> 418
    <212> PRT
    <213> Homo sapiens
    <220>
20 <221> Colligin 2
    <222> (1)..(418)
    <223> Accession No. as of 29 August 2003: P50454

    <400> 73

Met Arg Ser Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
1   5   10   15

Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr
        20   25   30

Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala
5   35   40   45

Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val
    50   55   60

Glu Asn Ile Leu Val Ser Pro Val Val Ala Ser Ser Leu Gly Leu
10 65   70   75   80

Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val
        85   90   95

Leu Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly
        100   105   110

Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp
15   115   120   125

Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp
        130   135   140

Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys
20 145   150   155   160

Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp
        165   170   175

Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val
        180   185   190

Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro
        195   200   205

His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe
        210   215   220

Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met His Arg Thr
5   225   230   235   240

Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Leu Gln Ile Val
        245   250   255

Glu Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro
10   260   265   270

His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu
    275   280   285

Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile
        290   295   300

Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His
15   305   310   315   320

Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp
        325   330   335

Leu Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe
        340   345   350

His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln
        355   360   365

Asp Ile Tyr Gly Arg Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala
    370   375   380

Asp His Pro Phe Ile Phe Leu Val Arg Arg Asp Thr Gln Ser Gly Ser Leu
385   390   395   400

Leu Phe Ile Gly Arg Leu Val Arg Pro Gly Asp Lys Met Arg Asp
                405   410   415

5   Glu Leu

<210> 74
10 <211> 263
    <212> PRT
    <213> Homo sapiens
    <220>
    <221> Chymotrypsinogen B precursor
15 <222> (1)..(263)
    <223> Accession No. as of 29 August 2003: P17538
    <400> 74

Met Ala Phe Leu Trp Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
20   1   5   10   15

Phe Gly Cys Gly Val Pro Ala Ile His Pro Val Leu Ser Gly Leu Ser
                20   25   30

Arg Ile Val Asn Gly Glu Asp Ala Val Pro Gly Ser Trp Pro Trp Gln
                35   40   45

Val Ser Leu Gln Asp Lys Thr Gly Phe His Phe Cys Gly Gly Ser Leu
                50   55   60

Ile Ser Glu Asp Trp Val Val Thr Ala Ala His Cys Gly Val Arg Thr
                65   70   75   80

5   Ser Asp Val Val Val Ala Gly Glu Phe Asp Gln Gly Ser Asp Glu Glu
                85   90   95

Asn Ile Gln Val Leu Lys Ile Ala Lys Val Phe Lys Asn Pro Lys Phe
                100   105   110

Ser Ile Leu Thr Val Asn Asn Asp Ile Thr Leu Leu Lys Leu Ala Thr
10   115   120   125

Pro Ala Arg Phe Ser Gln Thr Val Ser Ala Val Cys Leu Pro Ser Ala
                130   135   140

Asp Asp Asp Phe Pro Ala Gly Thr Leu Cys Ala Thr Thr Gly Trp Gly
145   150   155   160

15 Lys Thr Lys Tyr Asn Ala Asn Lys Thr Pro Asp Lys Leu Gln Gln Ala
                165   170   175

Ala Leu Pro Leu Leu Ser Asn Ala Glu Cys Lys Lys Ser Trp Gly Arg
                180   185   190

Arg Ile Thr Asp Val Met Ile Cys Ala Gly Ala Ser Gly Val Ser Ser
20   195   200   205

Cys Met Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Asp Gly Ala
                210   215   220

Trp Thr Leu Val Gly Ile Val Ser Trp Gly Ser Asp Thr Cys Ser Thr
225   230   235   240

Ser Ser Pro Gly Val Tyr Ala Arg Val Thr Lys Leu Ile Pro Trp Val
                        245   250   255
Gln Lys Ile Leu Ala Ala Asn
            260

<210> 75
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<221> Trypsin I precursor
<222> (1)..(247)
<223> Accession No. as of 29 August 2003: P07477

<400> 75

Met Asn Pro Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Leu Ala Ala
1   5   10   15
Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Glu Glu
                20   25   30
Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Tyr His Phe Cys
            35   40   45
Gly Gly Ser Leu Ile Asn Glu Gln Trp Val Val Ser Ala Gly His Cys
        50   55   60

Tyr Lys Ser Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val
                65   70   75   80
Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His
                        85   90   95
5   Pro Gln Tyr Asp Arg Lys Thr Leu Asn Asn Asp Ile Met Leu Ile Lys
                        100   105   110
Leu Ser Ser Arg Ala Val Ile Asn Ala Arg Val Ser Thr Ile Ser Leu
                115   120   125
Pro Thr Ala Pro Pro Ala Thr Gly Thr Lys Cys Leu Ile Ser Gly Trp
            130   135   140
10 Gly Asn Thr Ala Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys
    145   150   155   160
Leu Asp Ala Pro Val Leu Ser Gln Ala Lys Cys Glu Ala Ser Tyr Pro
                165   170   175
15 Gly Lys Ile Thr Ser Asn Met Phe Cys Val Gly Phe Leu Glu Gly Gly
            180   185   190
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly
                195   200   205
Gln Leu Gln Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Lys Asn
20 210   215   220
Lys Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Lys Trp Ile Lys
    225   230   235   240
Asn Thr Ile Ala Ala Asn Ser
            245

<210> 76
<211> 247
<212> PRT
<213> Homo sapiens
<220>
<221> Trypsin II precursor
<222> (1)..(247)
<223> Accession No. as of 29 August 2003: P07478
<400> 76

```
Met Asn Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Val Ala Ala
1               5                   10                  15
Pro Phe Asp Asp Asp Lys Ile Val Gly Gly Tyr Ile Cys Glu Glu
            20                  25                  30
Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Tyr His Phe Cys
            35                  40                  45
Gly Gly Ser Leu Ile Ser Glu Gln Trp Val Val Ser Ala Gly His Cys
50                  55                  60
Tyr Lys Ser Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val
65                  70                  75                  80
Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His
            85                  90                  95
```

```
Pro Lys Tyr Asn Ser Arg Thr Leu Asp Asn Asp Ile Leu Leu Ile Lys
                    100                 105                 110
Leu Ser Ser Pro Ala Val Ile Asn Ser Arg Val Ser Ala Ile Ser Leu
            115                 120                 125
Pro Thr Ala Pro Pro Ala Gly Thr Glu Ser Leu Ile Ser Gly Trp
5           130                 135                 140
Gly Asn Thr Leu Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys
            145                 150                 155             160
Leu Asp Ala Pro Val Leu Ser Gln Ala Glu Cys Glu Ala Ser Tyr Pro
10                  165                 170                 175
Gly Lys Ile Thr Asn Asn Met Phe Cys Val Gly Phe Leu Glu Gly Gly
                    180                 185                 190
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Ser Asn Gly
                    195                 200                 205
Glu Leu Gln Gly Ile Val Ser Trp Gly Tyr Gly Cys Ala Gln Lys Asn
15                  210                 215                 220
Arg Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Asp Trp Ile Lys
                    225                 230                 235             240
Asp Thr Ile Ala Ala Asn Ser
20                  245
```

<210> 77
<211> 379

```
        <212>  PRT

        <213>  Homo sapiens

        <220>

        <221>  Leukocyte elastase inhibitor (LEI)

 5      <222>  (1)..(379)

        <223>  Accession No. as of 29 August 2003: P30740

        <400>  77


        Met Glu Gln Leu Ser Ser Ala Asn Thr Arg Phe Ala Leu Asp Leu Phe
10      1               5                   10                  15

        Leu Ala Leu Ser Glu Asn Asn Pro Ala Gly Asn Ile Phe Ile Ser Pro
                    20                  25                  30

        Phe Ser Ile Ser Ser Ala Met Ala Met Val Phe Leu Gly Thr Arg Gly
                35                  40                  45

        Asn Thr Ala Ala Gln Leu Ser Lys Thr Phe His Phe Asn Thr Val Glu
15          50                  55                  60

        Glu Val His Ser Arg Phe Gln Ser Leu Asn Ala Asp Ile Asn Lys Arg
        65                  70                  75                  80

        Gly Ala Ser Tyr Ile Leu Lys Leu Ala Asn Arg Leu Tyr Gly Glu Lys
                        85                  90                  95

        Thr Tyr Asn Phe Leu Pro Glu Phe Leu Val Ser Thr Gln Lys Thr Tyr
20                      100                 105                 110

        Gly Ala Asp Leu Ala Ser Val Asp Phe Gln His Ala Ser Glu Asp Ala
                    115                 120                 125
```

```
        Arg Lys Thr Ile Asn Gln Trp Val Lys Gly Gln Thr Glu Gly Lys Ile
                        130                 135                 140

        Pro Glu Leu Leu Ala Ser Gly Met Val Asp Asn Met Thr Lys Leu Val
                        145                 150                 155                 160

        Leu Val Asn Ala Ile Tyr Phe Lys Gly Asn Trp Lys Asp Lys Phe Met
 5                      165                 170                 175

        Lys Glu Ala Thr Thr Asn Ala Pro Phe Arg Leu Asn Lys Lys Asp Arg
                                180                 185                 190

        Lys Thr Val Lys Met Met Tyr Gln Lys Lys Lys Phe Ala Tyr Gly Tyr
10                      195                 200                 205

        Ile Glu Asp Leu Lys Cys Arg Val Leu Glu Leu Pro Tyr Gln Gly Glu
                        210                 215                 220

        Glu Leu Ser Met Val Ile Leu Leu Pro Asp Asp Ile Glu Asp Glu Ser
                        225                 230                 235                 240

        Thr Gly Leu Lys Lys Ile Glu Glu Gln Leu Thr Leu Glu Lys Leu His
15                      245                 250                 255

        Glu Trp Thr Lys Pro Glu Asn Leu Asp Phe Ile Glu Val Asn Val Ser
                        260                 265                 270

        Leu Pro Arg Phe Lys Leu Glu Glu Ser Tyr Thr Leu Asn Ser Asp Leu
                        275                 280                 285

        Ala Arg Leu Gly Val Gln Asp Leu Phe Asn Ser Ser Lys Ala Asp Leu
20                      290                 295                 300

        Ser Gly Met Ser Gly Ala Arg Asp Ile Phe Ile Ser Lys Ile Val His
                        305                 310                 315                 320
```

Lys Ser Phe Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala
　　　　　　　325　　　　　　　330　　　　　　　335

Thr Ala Gly Ile Ala Thr Phe Cys Met Leu Met Pro Glu Glu Asn Phe
　　　　　　　340　　　　　　　345　　　　　　　350

Thr Ala Asp His Pro Phe Leu Phe Phe Ile Arg His Asn Ser Ser Gly
5　　　　　　　355　　　　　　　360　　　　　　　365

Ser Ile Leu Phe Leu Gly Arg Phe Ser Ser Pro
　　　　　　　370　　　　　　　375

10

<210> 78
<211> 573
<212> PRT
<213> Homo sapiens

15 <220>
<221> Hsp60
<222> (1)..(573)
<223> Accession No. as of 29 August 2003: P10809

<400> 78

20

Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg
1　　　　　5　　　　　　　　10　　　　　　　　15

Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe
　　　　　　　20　　　　　　　25　　　　　　　30

Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
　　　　　　　35　　　　　　　40　　　　　　　45

Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile
　　　　　　　50　　　　　　　55　　　　　　　60

5 Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val
65　　　　　　70　　　　　　　75　　　　　　　80

Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
　　　　　　　85　　　　　　　90　　　　　　　95

Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly
10　　　　　　100　　　　　　　105　　　　　　110

Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe
　　　　　　　115　　　　　　120　　　　　　125

Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
　　　　　　　130　　　　　　135　　　　　　140

15 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
145　　　　　　150　　　　　　155　　　　　　160

Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala
　　　　　　　165　　　　　　170　　　　　　175

Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys
20　　　　　　180　　　　　　　185　　　　　　190

Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
　　　　　　　195　　　　　　200　　　　　　205

Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
　　　　　　　210　　　　　　215　　　　　　220

Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
225   230   235   240

Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
        245   250   255

5   Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val
                260   265   270

Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu
        275   280   285

Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
10   290   295   300

Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
305   310   315   320

Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
        325   330   335

15   Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
                340   345   350

Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu
        355   360   365

Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu
20   370   375   380

Tyr Glu Lys Glu Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly
        385   390   395   400

Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
        405   410   415

Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
                420   425   430

Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile
        435   440   445

5   Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
                450   455   460

Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
        465   470   475   480

Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
10   485   490   495

Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn
        500   505   510

Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
        515   520   525

15   Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
                530   535   540

Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala
        545   550   555   560

Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
20   565   570

<210> 79

<211> 803

<212> PRT
<213> Homo sapiens
<220>
<221> Endoplasmin precursor (GRP94)
<222> (1)..(803)
<223> Accession No. as of 29 August 2003: P14625
<400> 79

```
    Met Arg Ala Leu Trp Val Leu Gly Leu Cys Cys Val Leu Leu Thr Phe
1                   5                   10                  15
    Gly Ser Val Arg Ala Asp Asp Glu Val Asp Val Asp Gly Thr Val Glu
                    20                  25                  30
    Glu Asp Leu Gly Lys Ser Arg Glu Gly Ser Arg Thr Asp Asp Glu Val
                35                  40                  45
15  Val Gln Arg Glu Glu Glu Ala Ile Gln Leu Asp Gly Leu Asn Ala Ser
            50                  55                  60
    Gln Ile Arg Glu Leu Arg Glu Lys Ser Glu Lys Phe Ala Phe Gln Ala
    65                  70                  75                  80
    Glu Val Asn Arg Met Met Lys Leu Ile Ile Asn Ser Leu Tyr Lys Asn
20                      85                  90                  95
    Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu
                        100                 105                 110
    Asp Lys Ile Arg Leu Ile Ser Leu Thr Asp Glu Asn Ala Leu Ser Gly
                115                 120                 125
```

```
    Asn Glu Glu Leu Thr Val Lys Ile Lys Cys Asp Lys Glu Lys Asn Leu
                    130                 135                 140
    Leu His Val Thr Asp Thr Gly Val Gly Met Thr Arg Glu Leu Val
    145                 150                 155                 160
5   Lys Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Glu Phe Leu Asn
                        165                 170                 175
    Lys Met Thr Glu Ala Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile
                    180                 185                 190
10  Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp Lys
                195                 200                 205
    Val Ile Val Thr Ser Lys His Asn Asn Asp Thr Gln His Ile Trp Glu
                    210                 215                 220
    Ser Asp Ser Asn Glu Phe Ser Val Ile Ala Asp Pro Arg Gly Asn Thr
15                  225                 230                 235         240
    Leu Gly Arg Gly Thr Thr Ile Thr Leu Val Leu Lys Glu Glu Ala Ser
                        245                 250                 255
    Asp Tyr Leu Glu Leu Asp Thr Ile Lys Asn Leu Val Lys Lys Tyr Ser
                    260                 265                 270
    Gln Phe Ile Asn Phe Pro Ile Tyr Val Trp Ser Ser Lys Thr Glu Thr
20                  275                 280                 285
    Val Glu Glu Pro Met Glu Glu Glu Glu Ala Ala Lys Glu Glu Lys Glu
                        290                 295                 300
    Glu Ser Asp Asp Glu Ala Ala Val Glu Glu Glu Glu Glu Glu Lys Lys
    305                 310                 315                 320
```

```
   Pro Lys Thr Lys Lys Val Glu Lys Thr Val Trp Asp Trp Glu Leu Met
                    325             330             335

   Asn Asp Ile Lys Pro Ile Trp Gln Arg Pro Ser Lys Glu Val Glu Glu
           340             345             350

 5 Asp Glu Tyr Lys Ala Phe Tyr Lys Ser Phe Ser Lys Glu Ser Asp Asp
               355             360             365

   Pro Met Ala Tyr Ile His Phe Thr Ala Glu Gly Glu Val Thr Phe Lys
       370             375             380

   Ser Ile Leu Phe Val Pro Thr Ser Ala Pro Arg Gly Leu Phe Asp Glu
10     385             390             395             400

   Tyr Gly Ser Lys Lys Ser Asp Tyr Ile Lys Leu Tyr Val Arg Arg Val
                   405             410             415

   Phe Ile Thr Asp Asp Phe His Asp Met Met Pro Lys Tyr Leu Asn Phe
               420             425             430

15 Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu Asn Val Ser Arg
                   435             440             445

   Glu Thr Leu Gln Gln His Lys Leu Leu Lys Val Ile Arg Lys Lys Leu
           450             455             460

   Val Arg Lys Thr Leu Asp Met Ile Lys Lys Ile Ala Asp Asp Lys Tyr
20 465             470             475             480

   Asn Asp Thr Phe Trp Lys Glu Phe Gly Thr Asn Ile Lys Leu Gly Val
               485             490             495

   Ile Glu Asp His Ser Asn Arg Thr Arg Leu Ala Lys Leu Leu Arg Phe
           500             505             510
```

```
   Gln Ser Ser His His Pro Thr Asp Ile Thr Ser Leu Asp Gln Tyr Val
                   515             520             525

   Glu Arg Met Lys Glu Lys Gln Asp Lys Ile Tyr Phe Met Ala Gly Ser
           530             535             540

 5 Ser Arg Lys Glu Ala Glu Ser Ser Pro Phe Val Glu Arg Leu Leu Lys
               545             550             555             560

   Lys Gly Tyr Glu Val Ile Tyr Leu Thr Glu Pro Val Asp Glu Tyr Cys
                       565             570             575

   Ile Gln Ala Leu Pro Glu Phe Asp Gly Lys Arg Phe Gln Asn Val Ala
10                 580             585             590

   Lys Glu Gly Val Lys Phe Asp Glu Ser Glu Lys Thr Lys Glu Ser Arg
                   595             600             605

   Glu Ala Val Glu Lys Glu Phe Glu Pro Leu Leu Asn Trp Met Lys Asp
               610             615             620

15 Lys Ala Leu Lys Asp Lys Ile Glu Lys Ala Val Val Ser Gln Arg Leu
                   625             630             635             640

   Thr Glu Ser Pro Cys Ala Leu Val Ala Ser Gln Tyr Gly Trp Ser Gly
                       645             650             655

   Asn Met Glu Arg Ile Met Lys Ala Gln Ala Tyr Gln Thr Gly Lys Asp
20                 660             665             670

   Ile Ser Thr Asn Tyr Tyr Ala Ser Gln Lys Lys Thr Phe Glu Ile Asn
               675             680             685

   Pro Arg His Pro Leu Ile Arg Asp Met Leu Arg Arg Ile Lys Glu Asp
           690             695             700
```

Glu Asp Lys Thr Val Leu Asp Ala Val Val Leu Phe Glu Thr
705   710   715   720

Ala Thr Leu Arg Ser Gly Tyr Leu Leu Pro Asp Thr Lys Ala Tyr Gly
725   730   735

Asp Arg Ile Glu Arg Met Leu Arg Leu Ser Asn Ile Asp Pro Asp
5   740   745   750

Ala Lys Val Glu Glu Glu Pro Glu Glu Pro Glu Glu Thr Ala Glu
755   760   765

Asp Thr Thr Glu Asp Thr Glu Gln Asp Glu Asp Glu Glu Met Asp Val
10   770   775   780

Gly Thr Asp Glu Glu Glu Thr Ala Lys Glu Ser Thr Ala Glu Lys
785   790   795   800

Asp Glu Leu

15

<210> 80
<211> 261
<212> PRT
20 <213> Homo sapiens
<220>
<221> Endoplasmic reticulum protein ERp29 precursor (ERp31)(ERp28)
<222> (1)..(261)
<223> Accession No. as of 29 August 2003: P30040

<400> 80

Met Ala Ala Ala Val Pro Arg Ala Ala Phe Leu Ser Pro Leu Leu Pro
1   5   10   15

Leu Leu Leu Gly Phe Leu Leu Leu Ser Ala Pro His Gly Gly Ser Gly
5   20   25   30

Leu His Thr Lys Gly Ala Leu Pro Leu Asp Thr Val Thr Phe Tyr Lys
35   40   45

Val Ile Pro Lys Ser Lys Phe Val Leu Val Lys Phe Asp Thr Gln Tyr
10   50   55   60

Pro Tyr Gly Glu Lys Gln Asp Glu Phe Lys Arg Leu Ala Glu Asn Ser
65   70   75   80

Ala Ser Ser Asp Asp Leu Leu Val Ala Glu Val Gly Ile Ser Asp Tyr
85   90   95

Gly Asp Lys Leu Asn Met Glu Leu Ser Glu Lys Tyr Lys Leu Asp Lys
15   100   105   110

Glu Ser Tyr Pro Val Phe Tyr Leu Phe Arg Asp Gly Asp Phe Glu Asn
115   120   125

Pro Val Pro Tyr Thr Gly Ala Val Lys Val Gly Ala Ile Gln Arg Trp
20   130   135   140

Leu Lys Gly Gln Gly Val Tyr Leu Gly Met Pro Gly Cys Leu Pro Val
145   150   155   160

Tyr Asp Ala Leu Ala Gly Glu Phe Ile Arg Ala Ser Gly Val Glu Ala
165   170   175

```
Arg Gln Ala Leu Leu Lys Gln Gly Asp Asn Leu Ser Ser Val Lys
                180                 185                 190

Glu Thr Gln Lys Trp Ala Glu Gln Tyr Leu Lys Ile Met Gly Lys
                195                 200                 205

Ile Leu Asp Gly Glu Asp Phe Ala Ser Glu Met Thr Arg Ile
5       210                 215                 220

Ala Arg Leu Ile Glu Lys Asn Lys Met Ser Asp Gly Lys Lys Glu Glu
                225                 230                 235             240

Leu Gln Lys Ser Leu Asn Ile Leu Thr Ala Phe Gln Lys Lys Gly Ala
10      245                 250                 255

Glu Lys Glu Glu Leu
        260
```

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15  <210>  81
    <211>  525
    <212>  PRT
    <213>  Homo sapiens
    <220>
20  <221>  Protein disulfide isomerase A2 precursor
    <222>  (1)..(525)
    <223>  Accession No. as of 29 August 2003: Q13087
    <400>  81
```

```
Met Ser Arg Gln Leu Leu Leu Pro Val Leu Leu Leu Leu Leu Arg Ala
1                5                   10                  15

Ser Cys Pro Trp Gly Gln Gln Gln Gly Ala Arg Ser Pro Ser Glu Glu
                20                  25                  30

Pro Pro Glu Glu Ile Pro Lys Glu Asp Gly Ile Leu Val Leu Ser
5       35                  40                  45

Arg His Thr Leu Gly Leu Ala Leu Arg Glu His Pro Ala Leu Leu Val
    50                  55                  60

Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Ala Pro Glu
                65                  70                  75              80

Tyr Ser Lys Ala Ala Ala Val Leu Ala Ala Glu Ser Met Val Val Thr
10                      85                  90                  95

Leu Ala Lys Val Asp Gly Pro Ala Gln Arg Glu Leu Ala Glu Glu Phe
                100                 105                 110

Gly Val Thr Glu Tyr Tyr Pro Thr Leu Lys Phe Phe Arg Asn Gly Asn Arg
15                  115                 120                 125

Thr His Pro Glu Glu Tyr Thr Gly Pro Arg Asp Ala Glu Gly Ile Ala
                130                 135                 140

Glu Trp Leu Arg Arg Arg Val Gly Pro Ser Ala Met Arg Leu Glu Asp
20  145                 150                 155                 160

Glu Ala Ala Ala Gln Ala Leu Ile Gly Gly Arg Asp Leu Val Val Ile
                165                 170                 175

Gly Phe Phe Gln Asp Leu Gln Asp Glu Asp Val Ala Thr Phe Leu Ala
                180                 185                 190
```

Leu Ala Gln Asp Ala Leu Asp Met Phe Gly Leu Thr Asp Arg Pro
      195   200   205

Arg Leu Phe Gln Gln Phe Gly Leu Thr Lys Asp Thr Val Leu Phe
      210   215   220

Lys Lys Phe Asp Glu Gly Arg Ala Asp Phe Asp Glu Glu Leu
5   225   230   235   240

Gly Leu Asp Leu Gly Asp Leu Ser Arg Phe Leu Val Thr His Ser Met
      245   250   255

Arg Leu Val Thr Glu Asn Ser Gln Thr Ser Ala Lys Ile Phe Ala
10   260   265   270

Ala Arg Ile Leu Asn His Leu Leu Leu Phe Val Asn Gln Thr Leu Ala
      275   280   285

Ala His Arg Glu Leu Leu Ala Gly Phe Gly Glu Ala Ala Pro Arg Phe
      290   295   300

Arg Gly Gln Val Leu Phe Val Val Asp Val Ala Ala Asp Asn Glu
15   305   310   315   320

His Val Leu Gln Tyr Phe Gly Leu Lys Ala Glu Ala Ala Pro Thr Leu
      325   330   335

Arg Leu Val Asn Leu Glu Thr Thr Lys Tyr Ala Pro Val Asp Gly
20   340   345   350

Gly Pro Val Thr Ala Ala Ser Ile Thr Ala Phe Cys His Ala Val Leu
      355   360   365

Asn Gly Gln Val Lys Pro Tyr Leu Leu Ser Gln Glu Ile Pro Pro Asp
      370   375   380

Trp Asp Gln Arg Pro Val Lys Thr Leu Val Gly Lys Asn Phe Glu Gln
      385   390   395   400

Val Ala Phe Asp Glu Lys Asn Val Phe Val Lys Phe Tyr Ala Pro
      405   410   415

Trp Cys Thr His Cys Lys Glu Met Ala Pro Ala Trp Glu Ala Leu Ala
5   420   425   430

Glu Lys Tyr Gln Asp His Glu Ile Ile Ala Glu Leu Asp Ala
      435   440   445

Thr Ala Asn Glu Leu Asp Ala Phe Ala Val His Gly Phe Pro Thr Leu
10   450   455   460

Lys Tyr Phe Pro Ala Gly Pro Gly Arg Lys Val Ile Glu Tyr Lys Ser
465   470   475   480

Thr Arg Asp Leu Glu Thr Phe Ser Lys Phe Leu Asp Asn Gly Gly Val
      485   490   495

Leu Pro Thr Glu Glu Pro Pro Glu Glu Pro Ala Ala Pro Phe Pro Glu
15   500   505   510

Pro Pro Ala Asn Ser Thr Met Gly Ser Lys Glu Glu Leu
      515   520   525

20

<210> 82
<211> 505
<212> PRT
<213> Homo sapiens

<220>

<221> Protein disulfide isomerase A3 precursor

<222> (1)..(505)

<223> Accession No. as of 29 August 2003: P30101

5   <400> 82

Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu
1   5   10   15

Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp
                20   25   30

10 Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met
            35   40   45

Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala
        50   55   60

15 Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu
65   70   75   80

Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly
                85   90   95

Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Asp Gly Glu Glu Ala
            100   105   110

20 Gly Ala Tyr Asp Gly Pro Arg Thr Ala Asp Gly Ile Val Ser His Leu
        115   120   125

Lys Lys Gln Ala Gly Pro Ala Ser Val Pro Leu Arg Thr Glu Glu Glu
    130   135   140

Phe Lys Phe Ile Ser Asp Lys Asp Ala Ser Ile Val Gly Phe Phe
        145   150   155   160

Asp Asp Ser Phe Ser Glu Ala His Ser Glu Phe Leu Lys Ala Ala Ser
                165   170   175

5   Asn Leu Arg Asp Asn Tyr Arg Phe Ala His Thr Asn Val Glu Ser Leu
            180   185   190

Val Asn Glu Tyr Asp Asp Asn Gly Glu Gly Ile Ile Leu Phe Arg Pro
                195   200   205

Ser His Leu Thr Asn Lys Phe Glu Asp Lys Thr Val Ala Tyr Thr Glu
10   210   215   220

Gln Lys Met Thr Ser Gly Lys Ile Lys Lys Phe Ile Gln Glu Asn Ile
                225   230   235   240

Phe Gly Ile Cys Pro His Met Thr Glu Asp Asn Lys Asp Leu Ile Gln
                245   250   255

15 Gly Lys Asp Leu Leu Ile Ala Tyr Tyr Asp Val Asp Tyr Glu Lys Asn
                260   265   270

Ala Lys Gly Ser Asn Tyr Trp Arg Asn Arg Val Met Met Val Ala Lys
                275   280   285

Lys Phe Leu Asp Ala Gly His Lys Leu Asn Phe Ala Val Ala Ser Arg
20   290   295   300

Lys Thr Phe Ser His Glu Leu Ser Asp Phe Gly Leu Glu Ser Thr Ala
                305   310   315   320

Gly Glu Ile Pro Val Val Ala Ile Arg Thr Ala Lys Gly Glu Lys Phe
                325   330   335

```
Val Met Gln Glu Glu Phe Ser Arg Gly Asp Lys Ala Leu Glu Arg Phe
                340                 345                 350
Leu Gln Asp Tyr Phe Asp Gly Asn Leu Lys Arg Tyr Leu Lys Ser Glu
                355                 360                 365
Pro Ile Pro Glu Ser Asn Asp Gly Pro Val Lys Val Val Val Ala Glu
 5              370                 375                 380
Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu
                385                 390                 395                 400
Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr
10              405                 410                 415
Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala
                420                 425                 430
Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg
                435                 440                 445
Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro
15              450                 455                 460
Lys Lys Tyr Glu Gly Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu
                465                 470                 475                 480
Gln Arg Glu Ala Thr Asn Pro Pro Val Ile Gln Glu Glu Lys Pro Lys
                485                 490                 495
Lys Lys Lys Lys Ala Gln Glu Asp Leu
20              500                 505
```

```
<210>  83
<211>  374
<212>  PRT
<213>  Homo sapiens

<220>
<221>  Alcohol dehydrogenase beta chain
<222>  (1)..(374)
<223>  Accession No. as of 29 August 2003: P00325

<400>  83
```

```
Ser Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp Glu
1               5                   10                  15
Val Lys Pro Phe Ser Ile Glu Asp Val Glu Val Ala Pro Lys
            20                  25                  30
Ala Tyr Glu Val Arg Ile Lys Met Val Ala Val Gly Ile Cys Arg Thr
15      35                  40                  45
Asp Asp His Val Val Ser Gly Asn Leu Val Thr Pro Leu Pro Val Ile
            50                  55                  60
Leu Gly His Glu Ala Ala Gly Ile Val Glu Ser Val Gly Glu Gly Val
65              70                  75                  80
Thr Thr Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Thr Pro Gln
                85                  90                  95
Cys Gly Lys Cys Arg Val Cys Lys Asn Pro Glu Ser Asn Tyr Cys Leu
            100                 105                 110
```

Lys Asn Asp Leu Gly Asn Pro Arg Gly Thr Leu Gln Asp Gly Thr Arg
               115   120   125

Arg Phe Thr Cys Arg Gly Lys Pro Ile His Phe Leu Gly Thr Ser
    130   135   140

5 Thr Phe Ser Gln Tyr Thr Val Val Asp Glu Asn Ala Val Ala Lys Ile
    145   150   155   160

Asp Ala Ala Ser Pro Glu Leu Lys Val Cys Leu Ile Gly Cys Gly Phe
               165   170   175

Ser Thr Gly Tyr Gly Ser Ala Val Asn Val Ala Lys Val Thr Pro Gly
10 180   185   190

Ser Thr Cys Ala Val Phe Gly Leu Gly Gly Val Gly Leu Ser Ala Val
               195   200   205

Met Gly Cys Lys Ala Ala Gly Ala Ala Arg Ile Ile Ala Val Asp Ile
15 210   215   220

Asn Lys Asp Lys Phe Ala Lys Ala Lys Glu Leu Gly Ala Thr Glu Cys
    225   230   235   240

Ile Asn Pro Gln Asp Tyr Lys Lys Pro Ile Gln Glu Val Leu Lys Glu
               245   250   255

Met Thr Asp Gly Gly Val Asp Phe Ser Phe Glu Val Ile Gly Arg Leu
20 260   265   270

Asp Thr Met Met Ala Ser Leu Leu Cys Cys His Glu Ala Cys Gly Thr
               275   280   285

Ser Val Ile Val Gly Val Pro Pro Ala Ser Gln Asn Leu Ser Ile Asn
    290   295   300

Pro Met Leu Leu Thr Gly Arg Thr Trp Lys Gly Ala Val Tyr Gly
    305   310   315   320

Gly Phe Lys Ser Lys Glu Gly Ile Pro Lys Val Ala Asp Phe Met
               325   330   335

5 Ala Lys Lys Phe Ser Leu Asp Ala Leu Ile Thr His Val Leu Pro Phe
               340   345   350

Glu Lys Ile Asn Glu Gly Phe Asp Leu Leu His Ser Gly Lys Ser Ile
               355   360   365

Arg Thr Val Leu Thr Phe
10 370

<210> 84
<211> 241
15 <212> PRT
<213> Homo sapiens
<220>
<221> Glutathione transferase omega 1
<222> (1)..(241)
20 <223> Accession No. as of 29 August 2003: P78417

<400> 84

Met Ser Gly Glu Ser Ala Arg Ser Leu Gly Lys Gly Ser Ala Pro Pro
1   5   10   15

```
Gly Pro Val Pro Glu Gly Ser Ile Arg Ile Tyr Ser Met Arg Phe Cys
                  20                    25                    30

Pro Phe Ala Glu Arg Thr Arg Leu Val Leu Lys Ala Lys Gly Ile Arg
                  35                    40                    45

5   His Glu Val Ile Asn Ile Asn Leu Asn Lys Pro Glu Trp Phe Phe
                50                    55                    60

Lys Lys Asn Pro Phe Gly Leu Val Pro Val Leu Glu Asn Ser Gln Gly
              65                    70                    75                    80

Gln Leu Ile Tyr Glu Ser Ala Ile Thr Cys Glu Tyr Leu Asp Glu Ala
10                85                    90                    95

Tyr Pro Gly Lys Leu Leu Pro Asp Asp Pro Tyr Glu Lys Ala Cys
              100                   105                   110

Gln Lys Met Ile Leu Glu Leu Phe Ser Lys Val Pro Ser Leu Val Gly
              115                   120                   125

15  Ser Phe Ile Arg Ser Gln Asn Lys Glu Asp Tyr Ala Gly Leu Lys Glu
              130                   135                   140

Glu Phe Arg Lys Glu Phe Thr Lys Leu Glu Glu Val Leu Thr Asn Lys
              145                   150                   155                   160

Lys Thr Thr Phe Phe Gly Gly Asn Ser Ile Ser Met Ile Asp Tyr Leu
20                165                   170                   175

Ile Trp Pro Trp Phe Glu Arg Leu Glu Ala Met Lys Leu Asn Glu Cys
              180                   185                   190

Val Asp His Thr Pro Lys Leu Lys Leu Trp Met Ala Ala Met Lys Glu
              195                   200                   205
```

```
Asp Pro Thr Val Ser Ala Leu Leu Thr Ser Glu Lys Asp Trp Gln Gly
              210                   215                   220

Phe Leu Glu Leu Tyr Leu Gln Asn Ser Pro Glu Ala Cys Asp Tyr Gly
              225                   230                   235

5   Leu
              240


<210> 85
10  <211> 999
<212> PRT
<213> Homo sapiens
<220>
<221> 150 kDa oxygen-regulated protein precursor (Orp150)
15  <222> (1)..(999)
<223> Accession No. as of 29 August 2003: Q9Y4L1
<400> 85

Met Ala Asp Lys Val Arg Arg Gln Arg Pro Arg Arg Val Cys Trp
20  1                 5                     10                    15

Ala Leu Val Ala Val Leu Leu Ala Asp Leu Ala Leu Ser Asp Thr
                    20                    25                    30

Leu Ala Val Met Ser Val Asp Leu Gly Ser Glu Ser Met Lys Val Ala
              35                    40                    45
```

Ile Val Lys Pro Gly Val Pro Met Glu Ile Val Leu Asn Lys Glu Ser
　　　　　　50　　　　　　55　　　　　　　　60

Arg Arg Lys Thr Pro Val Ile Val Thr Leu Lys Glu Asn Glu Arg Phe
65　　　　　　70　　　　　　　　75　　　　　　　　80

Phe Gly Asp Ser Ala Ser Met Ala Ile Lys Asn Pro Lys Ala Thr
　　　　　　　　85　　　　　　90　　　　　　　　95

Leu Arg Tyr Phe Gln His Leu Leu Gly Lys Gln Ala Asp Asn Pro His
　　　　　　　　100　　　　　105　　　　　　110

Val Ala Leu Tyr Gln Ala Arg Phe Pro Glu His Glu Leu Thr Phe Asp
10　　　　　　115　　　　　120　　　　　　125

Pro Gln Arg Gln Thr Val His Phe Gln Ile Ser Ser Gln Leu Gln Phe
　　　　　　　　130　　　　　135　　　　　　140

Ser Pro Glu Glu Val Leu Gly Met Val Leu Asn Tyr Ser Arg Ser Leu
145　　　　　　150　　　　　　155　　　　　　160

Ala Glu Asp Phe Ala Glu Gln Ile Lys Asp Ala Val Ile Thr Val
15　　　　　　165　　　　　170　　　　　　175

Pro Val Phe Phe Asn Gln Ala Glu Arg Arg Ala Val Leu Gln Ala Ala
　　　　　　　　180　　　　　185　　　　　　190

Arg Met Ala Gly Leu Lys Val Leu Gln Leu Ile Asn Asp Asn Thr Ala
20　　　　　　195　　　　　200　　　　　　205

Thr Ala Leu Ser Tyr Gly Val Phe Arg Arg Lys Asp Ile Asn Thr Thr
　　　　　　　　210　　　　　215　　　　　　220

Ala Gln Asn Ile Met Phe Tyr Asp Met Gly Ser Gly Ser Thr Val Cys
225　　　　　　230　　　　　　235　　　　　　240

Thr Ile Val Thr Tyr Gln Met Val Lys Thr Lys Glu Ala Gly Met Gln
　　　　　　　　245　　　　　250　　　　　　255

Pro Gln Leu Gln Ile Arg Gly Val Gly Phe Asp Arg Thr Leu Gly Gly
　　　　　　　　260　　　　　265　　　　　　270

Leu Glu Met Glu Leu Arg Arg Glu Arg Glu Leu Ala Gly Leu Phe Asn
5　　　　　　　275　　　　　280　　　　　　285

Glu Gln Arg Lys Gly Gln Arg Ala Lys Asp Val Arg Glu Asn Pro Arg
　　　　　　　　290　　　　　295　　　　　　300

Ala Met Ala Lys Leu Leu Arg Glu Ala Asn Arg Leu Lys Thr Val Leu
10　305　　　　　310　　　　　315　　　　　320

Ser Ala Asn Ala Asp His Met Ala Gln Ile Glu Gly Leu Met Asp Asp
　　　　　　　　325　　　　　330　　　　　　335

Val Asp Phe Lys Ala Lys Val Thr Arg Val Glu Phe Glu Glu Leu Cys
　　　　　　　　340　　　　　345　　　　　　350

Ala Asp Leu Phe Glu Arg Val Pro Gly Pro Val Gln Gln Ala Leu Gln
15　355　　　　　360　　　　　365

Ser Ala Glu Met Ser Leu Asp Glu Ile Glu Gln Val Ile Leu Val Gly
　　　　　　　　370　　　　　375　　　　　　380

Gly Ala Thr Arg Val Pro Arg Val Gln Glu Val Leu Leu Lys Ala Val
20　385　　　　　390　　　　　395　　　　　400

Gly Lys Glu Glu Leu Gly Lys Asn Ile Asn Ala Asp Glu Ala Ala Ala
　　　　　　　　405　　　　　410　　　　　　415

Met Gly Ala Val Tyr Gln Ala Ala Ala Leu Ser Lys Ala Phe Lys Val
　　　　　　　　420　　　　　425　　　　　　430

Lys Pro Phe Val Val Arg Asp Ala Val Val Tyr Pro Ile Leu Val Glu
     435   440   445

Phe Thr Arg Glu Val Glu Glu Pro Gly Ile His Ser Leu Lys His
     450   455   460

Asn Lys Arg Val Leu Phe Ser Arg Met Gly Pro Tyr Pro Gln Arg Lys
5   465   470   475   480

Val Ile Thr Phe Asn Arg Tyr Ser His Asp Phe Asn Phe His Ile Asn
     485   490   495

Tyr Gly Asp Leu Gly Phe Leu Gly Pro Glu Asp Leu Arg Val Phe Gly
10   500   505   510

Ser Gln Asn Leu Thr Thr Val Lys Leu Lys Gly Val Gly Asp Ser Phe
     515   520   525

Lys Lys Tyr Pro Asp Tyr Glu Ser Lys Gly Ile Lys Ala His Phe Asn
     530   535   540

Leu Asp Glu Ser Gly Val Leu Ser Leu Asp Arg Val Glu Ser Val Phe
15   545   550   555   560

Glu Thr Leu Val Glu Asp Ser Ala Glu Glu Ser Thr Leu Thr Lys
     565   570   575

Leu Gly Asn Thr Ile Ser Ser Leu Phe Gly Gly Thr Gly Thr Pro Asp
20   580   585   590

Ala Lys Glu Asn Gly Thr Asp Thr Val Gln Glu Glu Glu Ser Pro
     595   600   605

Ala Glu Gly Ser Lys Asp Glu Pro Gly Glu Gln Val Glu Leu Lys Glu
     610   615   620

Glu Ala Glu Ala Pro Val Glu Asp Gly Ser Gln Pro Pro Pro Glu
     625   630   635   640

Pro Lys Gly Asp Ala Thr Pro Glu Gly Glu Lys Ala Thr Glu Lys Glu
     645   650   655

Asn Gly Asp Lys Ser Glu Ala Gln Lys Pro Ser Glu Lys Ala Glu Ala
5   660   665   670

Gly Pro Glu Gly Val Ala Pro Ala Pro Gly Glu Lys Lys Gln Lys
     675   680   685

Pro Ala Arg Lys Arg Arg Met Val Glu Ile Gly Val Glu Leu Val
10   690   695   700

Val Leu Asp Leu Pro Glu Asp Lys Ala Gln Ser Val
     705   710   715   720

Gln Lys Leu Gln Asp Leu Thr Leu Arg Asp Glu Lys Gln Glu Arg
     725   730   735

Glu Lys Ala Ala Asn Ser Leu Glu Ala Phe Ile Phe Glu Thr Gln Asp
15   740   745   750

Lys Leu Tyr Gln Pro Glu Tyr Gln Glu Val Ser Thr Glu Gln Arg
     755   760   765

Glu Glu Ile Ser Gly Lys Leu Ser Ala Ala Ser Thr Trp Leu Glu Asp
20   770   775   780

Glu Gly Val Gly Ala Thr Thr Val Met Leu Lys Glu Lys Leu Ala Glu
     785   790   795   800

Leu Arg Lys Leu Cys Gln Gly Leu Phe Phe Arg Val Glu Glu Arg Lys
     805   810   815

Lys Trp Pro Glu Arg Leu Ser Ala Leu Asp Asn Leu Asn His Ser
            820   825   830

Ser Met Phe Leu Lys Gly Ala Arg Leu Ile Pro Glu Met Asp Gln Ile
            835   840   845

Phe Thr Glu Val Glu Met Thr Thr Leu Glu Lys Val Ile Asn Glu Thr
5   850   855   860

Trp Ala Trp Lys Asn Ala Thr Leu Ala Glu Gln Ala Lys Leu Pro Ala
            865   870   875   880

Thr Glu Lys Pro Val Leu Ser Lys Asp Ile Glu Ala Lys Met Met
            885   890   895

Ala Leu Asp Arg Glu Val Gln Tyr Leu Asn Lys Ala Lys Phe Thr
10   900   905   910

Lys Pro Arg Pro Arg Lys Asn Gly Thr Arg Ala Glu Pro
            915   920   925

Pro Leu Asn Ala Ser Ala Ser Asp Gln Gly Lys Val Ile Pro Pro
15   930   935   940

Ala Gly Gln Thr Glu Asp Ala Glu Pro Ile Ser Glu Pro Glu Lys Val
            945   950   955   960

Glu Thr Gly Ser Glu Pro Gly Asp Thr Glu Pro Leu Glu Leu Gly Gly
            965   970   975

Pro Gly Ala Glu Pro Glu Gln Lys Glu Gln Ser Thr Gly Gln Lys Arg
20   980   985   990

Pro Leu Lys Asn Asp Glu Leu
            995

<210> 86
<211> 271
<212> PRT
5   <213> Homo sapiens
<220>
<221> Peroxiredoxin 4
<222> (1)..(271)
10 <223> Accession No. as of 29 August 2003: Q13162
<400> 86

Met Glu Ala Leu Pro Leu Ala Ala Thr Thr Pro Asp His Gly Arg
1   5   10   15

His Arg Arg Leu Leu Leu Pro Leu Leu Phe Leu Leu Pro Ala
15   20   25   30

Gly Ala Val Gln Gly Trp Glu Thr Glu Glu Arg Pro Arg Thr Arg Glu
            35   40   45

Glu Glu Cys His Phe Tyr Ala Gly Gly Gln Val Tyr Pro Gly Glu Ala
20   50   55   60

Ser Arg Val Ser Val Ala Asp His Ser Leu His Leu Ser Lys Ala Lys
            65   70   75   80

Ile Ser Lys Pro Ala Pro Tyr Trp Glu Gly Thr Ala Val Ile Asp Gly
                85   90   95

Glu Phe Lys Glu Leu Lys Leu Thr Asp Tyr Arg Gly Lys Tyr Leu Val
                100   105   110

Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile
                115   120   125

Ile Ala Phe Gly Asp Arg Leu Glu Glu Phe Arg Ser Ile Asn Thr Glu
5   130   135   140

Val Val Ala Cys Ser Val Asp Ser Gln Phe Thr His Leu Ala Trp Ile
                145   150   155   160

Asn Thr Pro Arg Arg Gln Gly Gly Leu Gly Pro Ile Arg Ile Pro Leu
                165   170   175

Leu Ser Asp Leu Thr His Gln Ile Ser Lys Asp Tyr Gly Val Tyr Leu
10   180   185   190

Glu Asp Ser Gly His Thr Leu Arg Gly Leu Phe Ile Ile Asp Asp Lys
                195   200   205

Gly Ile Leu Arg Gln Ile Thr Leu Asn Asp Leu Pro Val Gly Arg Ser
15   210   215   220

Val Asp Glu Thr Leu Arg Leu Val Gln Ala Phe Gln Tyr Thr Asp Lys
225   230   235   240

His Gly Glu Val Cys Pro Ala Gly Trp Lys Pro Gly Ser Glu Thr Ile
                245   250   255

Ile Pro Asp Pro Ala Gly Lys Leu Lys Tyr Phe Asp Lys Leu Asn
20   260   265   270

<210> 87
<211> 288
<212> PRT
<213> Homo sapiens

5 <220>

   <221> MAWD binding protein

   <222> (1)..(288)

   <223> Accession No. as of 29 August 2003: P30039

   <400> 87

10

Met Lys Leu Pro Ile Phe Ile Ala Asp Ala Phe Thr Ala Arg Ala Phe
1   5   10   15

Arg Gly Asn Pro Ala Ala Val Cys Leu Leu Glu Asn Glu Leu Asp Glu
                20   25   30

Asp Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser Glu Thr Ala
15   35   40   45

Phe Ile Arg Lys Leu His Pro Thr Asp Asn Phe Ala Gln Ser Ser Cys
50   55   60

Phe Gly Leu Arg Trp Phe Thr Pro Ala Ser Glu Val Pro Leu Cys Gly
65   70   75   80

His Ala Thr Leu Ala Ser Ala Ala Val Leu Phe His Lys Ile Lys Asn
                85   90   95

Met Asn Ser Thr Leu Thr Phe Val Thr Leu Ser Gly Glu Leu Arg Ala
                100   105   110

<210> 88
<211> 511
<212> PRT
<213> Homo sapiens

<220>
<221> Alpha-amylase 2B precursor
<222> (1)..(511)
<223> Accession No. as of 29 August 2003: P19961

<400> 88

```
Met Lys Phe Phe Leu Leu Leu Phe Thr Ile Gly Phe Cys Trp Ala Gln
1               5                   10                  15

Tyr Ser Pro Asn Thr Gln Gln Gly Arg Thr Ser Ile Val His Leu Phe
            20                  25                  30

Glu Trp Arg Trp Val Asp Ile Ala Leu Glu Cys Glu Arg Tyr Leu Ala
        35                  40                  45

Pro Lys Gly Phe Gly Gly Val Gln Val Ser Pro Pro Asn Glu Asn Val
    50                  55                  60

Ala Ile His Asn Pro Phe Arg Pro Trp Trp Glu Arg Tyr Gln Pro Val
65                  70                  75                  80

Ser Tyr Lys Leu Cys Thr Arg Ser Gly Asn Glu Asp Glu Phe Arg Asn
            85                  90                  95

Met Val Thr Arg Cys Asn Asn Val Gly Val Arg Ile Tyr Val Asp Ala
            100                 105                 110
```

```
Arg Arg Ala Glu Asp Gly Ile Val Leu Asp Leu Tyr Pro Ala
                115                 120                 125

His Pro Gln Asp Phe His Glu Val Glu Asp Leu Ile Lys Thr Ala Ile
        130                 135                 140

Gly Asn Thr Leu Val Gln Asp Ile Cys Tyr Ser Pro Asp Thr Gln Lys
5                   145                 150                 155                 160

Leu Leu Val Arg Leu Ser Asp Val Tyr Asn Arg Ser Phe Glu Asn
                165                 170                 175

Leu Lys Val Asn Thr Glu Asn Leu Leu Gln Val Glu Asn Thr Gly Lys
10                  180                 185                 190

Val Lys Gly Leu Ile Leu Thr Leu Lys Gly Glu Pro Gly Gly Gln Thr
                195                 200                 205

Gln Ala Phe Asp Phe Tyr Ser Arg Tyr Phe Ala Pro Trp Val Gly Val
            210                 215                 220

Ala Glu Asp Pro Val Thr Gly Ser Ala His Ala Val Leu Ser Ser Tyr
15                  225                 230                 235                 240

Trp Ser Gln His Leu Gly Lys Lys Glu Met His Ala Phe Gln Cys Ser
            245                 250                 255

His Arg Gly Gly Glu Leu Gly Ile Leu Ser Arg Pro Asp Gly Arg Val
20                  260                 265                 270

Asp Ile Arg Gly Gly Ala Ala Val Leu Val Leu Glu Gly Thr Leu Thr Ala
                275                 280                 285
```

```
   Val Ile Asn His Met Ser Gly Asn Ala Val Ser Ala Gly Thr Ser Ser
                   115                 120                 125

   Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser Arg Asp Phe Pro Ala Val
                   130                 135                 140

 5 Pro Tyr Ser Gly Trp Asp Phe Asp Asn Asp Gly Lys Cys Thr Gly Ser
                   145                 150                 155                 160

   Gly Asp Ile Glu Asn Tyr Asn Asp Ala Thr Gln Val Arg Asp Cys Arg
                   165                 170                 175

   Leu Val Gly Leu Leu Asp Leu Ala Leu Glu Lys Asp Tyr Val Arg Ser
10                 180                 185                 190

   Lys Ile Ala Glu Tyr Met Asn His Leu Ile Asp Ile Gly Val Ala Gly
                   195                 200                 205

   Phe Arg Leu Asp Ala Ser Lys His Met Trp Pro Gly Asp Ile Lys Ala
                   210                 215                 220

15 Ile Leu Asp Lys Leu His Asn Leu Asn Ser Asn Trp Phe Pro Ala Gly
                   225                 230                 235                 240

   Ser Lys Pro Phe Ile Tyr Gln Glu Val Ile Asp Leu Gly Gly Glu Pro
                   245                 250                 255

   Ile Lys Ser Ser Asp Tyr Phe Gly Asn Gly Arg Val Thr Glu Phe Lys
20                 260                 265                 270

   Tyr Gly Ala Lys Leu Gly Thr Val Ile Arg Lys Trp Asn Gly Glu Lys
                   275                 280                 285

   Met Ser Tyr Leu Lys Asn Trp Gly Glu Gly Trp Gly Phe Met Pro Ser
                   290                 295                 300
```

```
   Asp Arg Ala Leu Val Phe Val Asp Asn His Asp Asn Gln Arg Gly His
                   305                 310                 315                 320

   Gly Ala Gly Gly Ala Ser Ile Leu Thr Phe Trp Asp Ala Arg Leu Tyr
                   325                 330                 335

 5 Lys Met Ala Val Gly Phe Met Leu Ala His Pro Tyr Gly Phe Thr Arg
                   340                 345                 350

   Val Met Ser Ser Tyr Arg Trp Pro Arg Gln Phe Gln Asn Gly Asn Asp
                   355                 360                 365

   Val Asn Asp Trp Val Gly Pro Pro Asn Asn Asn Gly Val Ile Lys Glu
10                 370                 375                 380

   Val Thr Ile Asn Pro Asp Thr Thr Cys Gly Asn Asp Trp Val Cys Glu
                   385                 390                 395                 400

   His Arg Trp Arg Gln Ile Arg Asn Met Val Asn Phe Arg Asn Val Val
                   405                 410                 415

15 Asp Gly Gln Pro Phe Thr Asn Trp Tyr Asp Asn Gly Ser Asn Gln Val
                   420                 425                 430

   Ala Phe Gly Arg Gly Asn Arg Gly Phe Ile Val Phe Asn Asn Asp Asp
                   435                 440                 445

   Trp Thr Phe Ser Leu Thr Leu Gln Thr Gly Leu Pro Ala Gly Thr Tyr
20                 450                 455                 460

   Cys Asp Val Ile Ser Gly Asp Lys Ile Asn Gly Asn Cys Thr Gly Ile
                   465                 470                 475                 480

   Lys Ile Tyr Val Ser Asp Asp Gly Lys Ala His Phe Ser Ile Ser Asn
                   485                 490                 495
```

Ser Ala Glu Asp Pro Phe Ile Ala Ile His Ala Glu Ser Lys Leu
            500   505   510

<210> 89
<211> 511
<212> PRT
<213> Homo sapiens
<220>
<221> Alpha-amylase, pancreatic precursor
<222> (1)..(511)
<223> Accession No. as of 29 August 2003: P04746
<400> 89

Met Lys Phe Phe Leu Leu Phe Thr Ile Gly Phe Cys Trp Ala Gln
1   5   10   15

Tyr Ser Pro Asn Thr Gln Gln Gly Arg Thr Ser Ile Val His Leu Phe
           20   25   30

Glu Trp Arg Trp Val Asp Ile Ala Leu Glu Cys Glu Arg Tyr Leu Ala
       35   40   45

Pro Lys Gly Phe Gly Gly Val Gln Val Ser Pro Pro Asn Glu Asn Val
     50   55   60

Ala Ile Tyr Asn Pro Phe Arg Pro Trp Trp Glu Arg Tyr Gln Pro Val
65   70   75   80

Ser Tyr Lys Leu Cys Thr Arg Ser Gly Asn Glu Asp Glu Phe Arg Asn
               85   90   95

Met Val Thr Arg Cys Asn Asn Val Gly Val Arg Ile Tyr Val Asp Ala
           100   105   110

Val Ile Asn His Met Cys Gly Asn Ala Val Ser Ala Gly Thr Ser Ser
       115   120   125

Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser Arg Asp Phe Pro Ala Val
     130   135   140

Pro Tyr Ser Gly Trp Asp Phe Asn Asp Gly Lys Cys Lys Thr Gly Ser
145   150   155   160

Gly Asp Ile Glu Asn Tyr Asn Asp Ala Thr Gln Val Arg Asp Cys Arg
             165   170   175

Leu Thr Gly Leu Leu Asp Leu Ala Leu Glu Lys Asp Tyr Val Arg Ser
         180   185   190

Lys Ile Ala Glu Tyr Met Asn His Leu Ile Asp Ile Gly Val Ala Gly
      195   200   205

Phe Arg Leu Asp Ala Ser Lys His Met Trp Pro Gly Asp Ile Lys Ala
    210   215   220

Ile Leu Asp Lys Leu His Asn Leu Asn Ser Asn Trp Phe Pro Ala Gly
225   230   235   240

Ser Lys Pro Phe Ile Tyr Gln Glu Val Ile Asp Leu Gly Gly Glu Pro
          245   250   255

Ile Lys Ser Ser Asp Tyr Phe Gly Asn Gly Arg Val Thr Glu Phe Lys
       260   265   270

```
   Tyr Gly Ala Lys Leu Gly Thr Val Ile Arg Lys Trp Asn Gly Glu Lys
                   275                 280                 285

   Met Ser Tyr Leu Lys Asn Trp Gly Glu Gly Trp Gly Phe Val Pro Ser
               290                 295                 300

 5 Asp Arg Ala Leu Val Phe Val Asp Asn His Asp Asn Gln Arg Gly His
           305                 310                 315                 320

   Gly Ala Gly Gly Ala Ser Ile Leu Thr Phe Trp Asp Ala Arg Leu Tyr
                   325                 330                 335

   Lys Met Ala Val Gly Phe Met Leu Ala His Pro Tyr Gly Phe Thr Arg
10                 340                 345                 350

   Val Met Ser Ser Tyr Arg Trp Pro Arg Gln Phe Gln Asn Gly Asn Asp
                   355                 360                 365

   Val Asn Asp Trp Val Gly Pro Pro Asn Asn Asn Gly Val Ile Lys Glu
               370                 375                 380

15 Val Thr Ile Asn Pro Asp Thr Thr Cys Gly Asn Asp Trp Val Cys Glu
           385                 390                 395                 400

   His Arg Trp Arg Gln Ile Arg Asn Met Val Ile Phe Arg Asn Val Val
               405                 410                 415

   Asp Gly Gln Pro Phe Thr Asn Trp Tyr Asp Asn Gly Ser Asn Gln Val
20                 420                 425                 430

   Ala Phe Gly Arg Gly Asn Arg Gly Phe Ile Val Phe Asn Asn Asp Asp
               435                 440                 445

   Trp Ser Phe Ser Leu Thr Leu Gln Thr Gly Leu Pro Ala Gly Thr Tyr
           450                 455                 460
```

```
   Cys Asp Val Ile Ser Gly Asp Lys Ile Asn Gly Asn Cys Thr Gly Ile
           465                 470                 475                 480

   Lys Ile Tyr Val Ser Asp Asp Gly Lys Ala His Phe Ser Ile Ser Asn
               485                 490                 495

 5 Ser Ala Glu Asp Pro Phe Ile Ala Ile His Ala Glu Ser Lys Leu
               500                 505                 510


   <210> 90
10 <211> 553
   <212> PRT
   <213> Homo sapiens
   <220>
   <221> ATP synthase alpha chain
15 <222> (1)..(553)
   <223> Accession No. as of 29 August 2003: P25705
   <400> 90

   Met Leu Ser Val Arg Val Ala Ala Ala Val Val Arg Ala Leu Pro Arg
20 1               5                   10                  15

   Arg Ala Gly Leu Val Ser Arg Asn Ala Leu Gly Ser Ser Phe Ile Ala
               20                  25                  30

   Ala Arg Asn Phe His Ala Ser Asn Thr His Leu Gln Lys Thr Gly Thr
           35                  40                  45
```

Ala Glu Met Ser Ser Ile Leu Glu Arg Ile Leu Gly Ala Asp Thr
          50   55   60

Ser Val Asp Leu Glu Glu Thr Gly Arg Val Leu Ser Ile Gly Asp Gly
          65   70   75   80

5   Ile Ala Arg Val His Gly Leu Arg Asn Val Gln Ala Glu Glu Met Val
          85   90   95

Glu Phe Ser Ser Gly Leu Lys Gly Met Ser Leu Asn Leu Glu Pro Asp
          100   105   110

Asn Val Gly Val Val Phe Gly Asn Asp Lys Leu Ile Lys Glu Gly
10   115   120   125

Asp Ile Val Lys Arg Thr Gly Ala Ile Val Asp Val Pro Val Gly Glu
          130   135   140

Glu Leu Leu Gly Arg Val Val Asp Ala Leu Gly Asn Ala Ile Asp Gly
          145   150   155   160

15 Lys Gly Pro Ile Gly Ser Lys Thr Arg Arg Arg Val Gly Leu Lys Ala
          165   170   175

Pro Gly Ile Ile Pro Arg Ile Ser Val Arg Glu Pro Met Gln Thr Gly
          180   185   190

Ile Lys Ala Val Asp Ser Leu Val Pro Ile Gly Arg Gly Gln Arg Glu
          195   200   205

20 Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr Ser Ile Ala Ile Asp
          210   215   220

Thr Ile Ile Asn Gln Lys Arg Phe Asn Asp Gly Ser Asp Glu Lys Lys
          225   230   235   240

Lys Leu Tyr Cys Ile Tyr Val Ala Ile Gly Gln Lys Arg Ser Thr Val
          245   250   255

Ala Gln Leu Val Lys Arg Leu Thr Asp Ala Asp Ala Met Lys Tyr Thr
          260   265   270

5   Ile Val Ser Ala Thr Ser Asp Ala Ala Pro Leu Gln Tyr Leu
          275   280   285

Ala Pro Tyr Ser Gly Cys Ser Met Gly Glu Tyr Phe Arg Asp Asn Gly
          290   295   300

Lys His Ala Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala
10 305   310   315   320

Tyr Arg Gln Met Ser Leu Leu Leu Arg Arg Pro Gly Arg Glu Ala
          325   330   335

Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala
          340   345   350

15 Ala Lys Met Asn Asp Ala Phe Gly Gly Gly Ser Leu Thr Ala Leu Pro
          355   360   365

Val Ile Glu Thr Gln Ala Gly Asp Val Ser Ala Tyr Ile Pro Thr Asn
          370   375   380

Val Ile Ser Ile Thr Asp Gly Gln Ile Phe Leu Glu Thr Glu Leu Phe
20 385   390   395   400

Tyr Lys Gly Ile Arg Pro Ala Ile Asn Val Gly Leu Ser Val Ser Arg
          405   410   415

Val Gly Ser Ala Ala Gln Thr Arg Ala Met Lys Gln Val Ala Gly Thr
          420   425   430

```
Met Lys Leu Glu Leu Ala Gln Tyr Arg Glu Val Ala Ala Phe Ala Gln
                435                 440                 445

Phe Gly Ser Asp Leu Asp Ala Ala Thr Gln Gln Leu Leu Ser Arg Gly
                450                 455                 460

Val Arg Leu Thr Glu Leu Leu Lys Gln Gly Gln Tyr Ser Pro Met Ala
5               465                 470                 475                 480

Ile Glu Glu Gln Val Ala Val Ile Tyr Ala Gly Val Arg Gly Tyr Leu
                485                 490                 495

Asp Lys Leu Glu Pro Ser Lys Ile Thr Lys Phe Glu Asn Ala Phe Leu
10              500                 505                 510

Ser His Val Ser Gln His Gln Ala Leu Leu Gly Thr Ile Arg Ala
                515                 520                 525

Asp Gly Lys Ile Ser Glu Gln Ser Asp Ala Lys Leu Lys Glu Ile Val
15              530                 535                 540

Thr Asn Phe Leu Ala Gly Phe Glu Ala
                545                 550
```

<210> 91

20 <211> 742

<212> PRT

<213> Homo sapiens

<220>

<221> Bile-salt-activated lipase precursor

<222> (1)..(742)

<223> Accession No. as of 29 August 2003: P19835

<400> 91

```
Met Gly Arg Leu Gln Leu Val Val Leu Gly Leu Thr Cys Cys Trp Ala
5   1               5                   10                  15

Val Ala Ser Ala Ala Lys Leu Gly Ala Val Tyr Thr Glu Gly Gly Phe
                20                  25                  30

Val Glu Gly Val Asn Lys Lys Leu Gly Leu Leu Gly Asp Ser Val Asp
10              35                  40                  45

Ile Phe Lys Gly Ile Pro Phe Ala Ala Pro Thr Lys Ala Leu Glu Asn
                50                  55                  60

Pro Gln Pro His Pro Gly Trp Gln Gly Thr Leu Lys Ala Lys Asn Phe
65                  70                  75                  80

Lys Lys Arg Cys Leu Gln Ala Thr Ile Thr Gln Asp Ser Thr Tyr Gly
15              85                  90                  95

Asp Glu Asp Cys Leu Tyr Leu Asn Ile Trp Val Pro Gln Gly Arg Lys
                100                 105                 110

Gln Val Ser Arg Asp Leu Pro Val Met Ile Trp Ile Tyr Gly Gly Ala
20              115                 120                 125

Phe Leu Met Gly Ser Gly His Gly Ala Asn Phe Leu Asn Asn Tyr Leu
                130                 135                 140

Tyr Asp Gly Glu Glu Ile Ala Thr Arg Gly Asn Val Ile Val Val Thr
                145                 150                 155                 160
```

```
Asn Lys Asn Lys Val Thr Glu Glu Asp Phe Tyr Lys Leu Val
                       355                 360                 365

Ser Glu Phe Thr Ile Thr Lys Gly Leu Arg Gly Ala Lys Thr Thr Phe
                       370                 375                 380

5   Asp Val Tyr Thr Glu Ser Trp Ala Gln Asp Pro Ser Gln Glu Asn Lys
                       385                 390                 395                 400

    Lys Lys Thr Val Asp Phe Glu Thr Asp Val Leu Phe Leu Val Pro
                       405                 410                 415

10  Thr Glu Ile Ala Leu Ala Gln His Arg Ala Asn Ala Lys Ser Ala Lys
                       420                 425                 430

    Thr Tyr Ala Tyr Leu Phe Ser His Pro Ser Arg Met Pro Val Tyr Pro
                       435                 440                 445

    Lys Trp Val Gly Ala Asp His Ala Asp Asp Ile Gln Tyr Val Phe Gly
                       450                 455                 460

15  Lys Pro Phe Ala Thr Pro Thr Gly Tyr Arg Pro Gln Asp Arg Thr Val
                       465                 470                 475                 480

    Ser Lys Ala Met Ile Ala Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp
                       485                 490                 495

20  Pro Asn Met Gly Asp Ser Ala Val Pro Thr His Trp Glu Pro Tyr Thr
                       500                 505                 510

    Thr Glu Asn Ser Gly Tyr Leu Glu Ile Thr Lys Lys Met Gly Ser Ser
                       515                 520                 525

    Ser Met Lys Arg Ser Leu Arg Thr Arg Asn Phe Leu Arg Tyr Trp Thr Leu
                       530                 535                 540
```

```
Phe Asn Tyr Arg Val Gly Pro Leu Gly Phe Leu Ser Thr Gly Asp Ala
                       165                 170                 175

Asn Leu Pro Gly Asn Tyr Gly Leu Arg Asp Gln His Met Ala Ile Ala
                       180                 185                 190

5   Trp Val Lys Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Asn Asn Ile
                       195                 200                 205

    Thr Leu Phe Gly Glu Ser Ala Gly Gly Ala Ser Val Ser Leu Gln Thr
                       210                 215                 220

10  Leu Ser Pro Tyr Asn Lys Gly Leu Ile Arg Arg Ala Ile Ser Gln Ser
                       225                 230                 235                 240

    Gly Val Ala Leu Ser Pro Trp Val Ile Gln Lys Asn Pro Leu Phe Trp
                       245                 250                 255

    Ala Lys Lys Val Ala Glu Lys Val Gly Cys Pro Val Gly Asp Ala Ala
                       260                 265                 270

15  Arg Met Ala Gln Cys Leu Lys Val Thr Asp Pro Arg Ala Leu Thr Leu
                       275                 280                 285

    Ala Tyr Lys Val Pro Leu Ala Gly Leu Glu Tyr Pro Met Leu His Tyr
                       290                 295                 300

20  Val Gly Phe Val Pro Val Ile Asp Gly Asp Phe Ile Pro Ala Asp Pro
                       305                 310                 315                 320

    Ile Asn Leu Tyr Ala Asn Ala Ala Asp Ile Asp Tyr Ile Ala Gly Thr
                       325                 330                 335

    Asn Asn Met Asp Gly His Ile Phe Ala Ser Ile Asp Met Pro Ala Ile
                       340                 345                 350
```

Thr Tyr Ala Leu Pro Thr Val Thr Asp Gln Glu Ala Thr Pro Val
    545   550   555   560

Pro Pro Thr Gly Asp Ser Glu Ala Thr Pro Val Pro Pro Thr Gly Asp
        565   570   575

 5 Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro
            580   585   590

Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly
        595   600   605

Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro
10   610   615   620

Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr
        625   630   635   640

Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala
        645   650   655

15 Pro Pro Val Pro Pro Thr Gly Asp Ala Gly Pro Pro Pro Val Pro Pro
            660   665   670

Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly
        675   680   685

Ala Pro Pro Val Thr Pro Thr Gly Asp Ser Glu Thr Ala Pro Val Pro
20   690   695   700

Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser
        705   710   715   720

Glu Ala Ala Pro Val Pro Pro Thr Asp Ser Lys Glu Ala Gln Met
        725   730   735

Pro Ala Val Ile Arg Phe
                740

 5 <210> 92
    <211> 467
    <212> PRT
    <213> Homo sapiens
    <220>
10 <221> Pancreatic lipase related protein precursor
    <222> (1)..(467)
    <223> Accession No. as of 29 August 2003: P54315
    <400> 92

15 Met Leu Ile Phe Trp Thr Ile Thr Leu Phe Leu Leu Gly Ala Ala Lys
    1   5   10   15

Gly Lys Glu Val Cys Tyr Glu Asp Leu Gly Cys Phe Ser Asp Thr Glu
        20   25   30

Pro Trp Gly Thr Ala Ile Arg Pro Lys Ile Leu Leu Pro Trp Ser
20   35   40   45

Pro Glu Lys Ile Gly Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro
        50   55   60

Asn Asn Phe Gln Ile Leu Leu Leu Ser Asp Pro Ser Thr Ile Glu Ala
        65   70   75   80

```
   Ser Asn Phe Gln Met Asp Arg Lys Thr Arg Phe Ile Ile His Gly Phe
                     85                90                95

   Ile Asp Lys Gly Asp Glu Ser Trp Val Thr Asp Met Cys Lys Lys Leu
                     100               105               110

 5 Phe Glu Val Glu Val Asn Cys Ile Cys Val Asp Trp Lys Lys Gly
                     115               120               125

   Ser Gln Ala Thr Tyr Thr Gln Ala Ala Asn Asn Val Arg Val Val Gly
                     130               135               140

10 Ala Gln Val Ala Gln Met Leu Asp Ile Leu Leu Thr Glu Tyr Ser Tyr
   145               150               155               160

   Pro Pro Ser Lys Val His Leu Ile Gly His Ser Leu Gly Ala His Val
                     165               170               175

   Ala Gly Glu Ala Gly Ser Lys Thr Pro Gly Leu Ser Arg Ile Thr Gly
                     180               185               190

15 Leu Asp Pro Val Glu Ala Ser Phe Glu Ser Thr Pro Glu Glu Val Arg
                     195               200               205

   Leu Asp Pro Ser Asp Ala Asp Phe Val Asp Val Ile His Thr Asp Ala
                     210               215               220

20 Ala Pro Leu Ile Pro Phe Leu Gly Phe Gly Thr Asn Gln Gln Met Gly
   225               230               235               240

   His Leu Asp Phe Phe Pro Asn Gly Gly Glu Ser Met Pro Gly Cys Lys
                     245               250               255

   Lys Asn Ala Leu Ser Gln Ile Val Asp Leu Asp Gly Ile Trp Ala Gly
                     260               265               270
```

```
   Thr Arg Asp Phe Val Ala Cys Asn His Leu Arg Ser Lys Tyr Tyr
                     275               280               285

   Leu Glu Ser Ile Leu Asn Pro Asp Gly Phe Ala Ala Tyr Pro Cys Thr
                     290               295               300

 5 Ser Tyr Lys Ser Phe Glu Ser Asp Lys Cys Phe Pro Cys Pro Asp Gln
   305               310               315               320

   Gly Cys Pro Gln Met Gly His Tyr Ala Asp Lys Phe Ala Gly Arg Thr
                     325               330               335

   Ser Glu Gln Gln Lys Phe Phe Leu Asn Thr Gly Glu Ala Ser Asn
10                   340               345               350

   Phe Ala Arg Trp Arg Tyr Gly Val Ser Ile Thr Leu Ser Gly Arg Thr
                     355               360               365

   Ala Thr Gly Gln Ile Lys Val Ala Leu Phe Gly Asn Lys Gly Asn Thr
                     370               375               380

15 His Gln Tyr Ser Ile Phe Arg Gly Ile Leu Lys Pro Gly Ser Thr His
   385               390               395               400

   Ser Tyr Glu Phe Asp Ala Lys Leu Asp Val Gly Thr Ile Glu Lys Val
                     405               410               415

   Lys Phe Leu Trp Asn Asn Val Ile Asn Pro Thr Leu Pro Lys Val
20                   420               425               430

   Gly Ala Thr Lys Ile Thr Val Gln Lys Gly Glu Glu Lys Thr Val Tyr
                     435               440               445

   Asn Phe Cys Ser Glu Asp Thr Val Arg Glu Asp Thr Leu Leu Thr Leu
                     450               455               460
```

Thr Pro Cys
465

<210> 93
<211> 469
<212> PRT
<213> Homo sapiens
<220>
<221> Pancreatic lipase related protein 2 precursor
<222> (1)..(469)
<223> Accession No. as of 29 August 2003: P54317
<400> 93

Met Leu Pro Pro Trp Thr Leu Gly Leu Leu Leu Leu Ala Thr Val Arg
1   5   10   15

Gly Lys Glu Val Cys Tyr Gly Gln Leu Gly Cys Phe Ser Asp Glu Lys
                20   25   30

Pro Trp Ala Gly Thr Leu Gln Arg Pro Val Lys Leu Leu Pro Trp Ser
            35   40   45

Pro Glu Asp Ile Asp Thr Arg Phe Leu Tyr Thr Asn Glu Asn Pro
        50   55   60

Asn Asn Phe Gln Leu Ile Thr Gly Thr Glu Pro Asp Thr Ile Glu Ala
65   70   75   80

Ser Asn Phe Gln Leu Asp Asp Arg Lys Thr Arg Phe Ile Ile His Gly Phe
                    85   90   95

Leu Asp Lys Ala Glu Asp Ser Trp Pro Ser Asp Met Cys Lys Met
                    100   105   110

Phe Glu Val Glu Lys Val Asn Cys Ile Cys Val Asp Trp Arg His Gly
5   115   120   125

Ser Arg Ala Met Tyr Thr Gln Ala Val Gln Asn Ile Arg Val Val Gly
                    130   135   140

Ala Glu Thr Ala Phe Leu Ile Gln Ala Leu Ser Thr Gln Leu Gly Tyr
10 145   150   155   160

Ser Leu Glu Asp Val His Val Ile Gly His Ser Leu Gly Ala His Thr
                    165   170   175

Ala Ala Glu Ala Gly Arg Arg Leu Gly Gly Arg Val Gly Arg Ile Thr
                    180   185   190

Gly Leu Asp Pro Ala Gly Pro Cys Phe Gln Asp Glu Pro Glu Glu Val
15   195   200   205

Arg Leu Asp Pro Ser Asp Ala Val Phe Val Asp Val Ile His Thr Asp
                    210   215   220

Ser Ser Pro Ile Val Pro Ser Leu Gly Phe Gly Met Ser Gln Lys Val
20 225   230   235   240

Gly His Leu Asp Phe Pro Asn Gly Gly Lys Glu Met Pro Gly Cys
                    245   250   255

Lys Lys Asn Val Leu Ser Thr Ile Thr Asp Ile Asp Gly Ile Trp Glu
                    260   265   270

Ser Leu Tyr Pro Cys

  465

<210> 94

<211> 465

<212> PRT

<213> Homo sapiens

<220>

<221> Triacylglycerol lipase, pancreatic precursor

<222> (1)..(465)

<223> Accession No. as of 29 August 2003: P16233

<400> 94

Met Leu Pro Leu Trp Thr Leu Ser Leu Leu Leu Gly Ala Val Ala Gly
1   5   10   15

Lys Glu Val Cys Tyr Glu Arg Leu Gly Cys Phe Ser Asp Asp Ser Pro
               20   25   30

Trp Ser Gly Ile Thr Glu Arg Pro Leu His Ile Leu Pro Trp Ser Pro
        35   40   45

Lys Asp Val Asn Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro Asn
    50   55   60

Asn Phe Gln Glu Val Ala Ala Asp Ser Ser Ser Ile Ser Gly Ser Asn
65   70   75   80

Gly Ile Gly Gly Phe Val Ser Cys Asn His Leu Arg Ser Phe Glu Tyr
        275   280   285

Tyr Ser Ser Ser Val Leu Asn Pro Asp Gly Phe Leu Gly Tyr Pro Cys
    290   295   300

Ala Ser Tyr Asp Glu Gln Glu Ser Cys Lys Cys Phe Cys Pro Ala
305   310   315   320

Glu Gly Cys Pro Lys Met Gly His Tyr Ala Asp Gln Phe Lys Gly Lys
              325   330   335

Thr Ser Ala Val Glu Gln Thr Phe Phe Leu Asn Thr Gly Glu Ser Gly
        340   345   350

Asn Phe Thr Ser Trp Arg Tyr Lys Val Ser Val Thr Leu Ser Gly Lys
              355   360   365

Glu Lys Val Asn Gly Tyr Ile Arg Ile Ala Leu Tyr Gly Ser Asn Glu
    370   375   380

Asn Ser Lys Gln Tyr Glu Ile Phe Lys Gly Ser Leu Lys Pro Asp Ala
385   390   395   400

Ser His Thr Cys Ala Ile Asp Val Asp Phe Asn Val Gly Lys Ile Gln
              405   410   415

Lys Val Lys Phe Leu Trp Asn Lys Arg Gly Ile Asn Leu Ser Glu Pro
    420   425   430

Lys Leu Gly Ala Ser Gln Ile Thr Val Gln Ser Gly Glu Asp Gly Thr
        435   440   445

Glu Tyr Asn Phe Cys Ser Ser Asp Thr Val Glu Glu Asn Val Leu Gln
450   455   460

Phe Lys Thr Asn Arg Lys Thr Arg Phe Ile His Gly Phe Ile Asp
                85   90   95

Lys Gly Glu Asn Trp Leu Ala Asn Val Cys Lys Asn Leu Phe Lys
             100   105   110

5 Val Glu Ser Val Asn Cys Ile Cys Val Asp Trp Lys Gly Gly Ser Arg
             115   120   125

Thr Gly Tyr Thr Gln Ala Ser Gln Asn Ile Arg Ile Val Gly Ala Glu
             130   135   140

Val Ala Tyr Phe Val Glu Phe Leu Gln Ser Ala Phe Gly Tyr Ser Pro
10 145   150   155   160

Ser Asn Val His Val Ile Gly His Ser Leu Gly Ala His Ala Ala Gly
             165   170   175

Glu Ala Gly Arg Arg Thr Asn Gly Thr Ile Gly Arg Ile Thr Gly Leu
             180   185   190

15 Asp Pro Ala Glu Pro Cys Phe Gln Gly Thr Pro Glu Leu Val Arg Leu
             195   200   205

Asp Pro Ser Asp Ala Lys Phe Val Asp Val Ile His Thr Asp Gly Ala
             210   215   220

Pro Ile Val Pro Asn Leu Gly Phe Gly Met Ser Gln Val Val Gly His
20 225   230   235   240

Leu Asp Phe Phe Pro Asn Gly Gly Val Glu Met Pro Gly Cys Lys Lys
             245   250   255

Asn Ile Leu Ser Gln Ile Val Asp Ile Asp Gly Ile Trp Glu Gly Thr
             260   265   270

Arg Asp Phe Ala Ala Cys Asn His Leu Arg Ser Lys Tyr Tyr Thr
             275   280   285

Asp Ser Ile Val Asn Pro Asp Gly Phe Ala Gly Phe Pro Cys Ala Ser
             290   295   300

5 Tyr Asn Val Phe Thr Ala Asn Lys Cys Phe Pro Cys Pro Ser Gly Gly
             305   310   315   320

Cys Pro Gln Met Gly His Tyr Ala Asp Arg Tyr Pro Gly Lys Thr Asn
             325   330   335

Asp Val Gly Gln Lys Phe Tyr Leu Asp Thr Gly Asp Ala Ser Asn Phe
10 340   345   350

Ala Arg Trp Arg Tyr Lys Val Ser Val Thr Leu Ser Gly Lys Lys Val
             355   360   365

Thr Gly His Ile Leu Val Ser Leu Phe Gly Asn Lys Gly Asn Ser Lys
             370   375   380

15 Gln Tyr Glu Ile Phe Lys Gly Thr Leu Lys Pro Asp Ser Thr His Ser
             385   390   395   400

Asn Glu Phe Asp Ser Asp Val Asp Leu Gln Met Val Lys
             405   410   415

Phe Ile Trp Tyr Asn Asn Val Ile Asn Pro Thr Leu Pro Arg Val Gly
20   420   425   430

Ala Ser Lys Ile Ile Val Glu Thr Asn Val Gly Lys Gln Phe Asn Phe
             435   440   445

Cys Ser Pro Glu Thr Val Arg Glu Glu Val Leu Leu Thr Leu Thr Pro
             450   455   460

Cys
465

<210> 95
<211> 572
<212> PRT
<213> Homo sapiens
<220>
<221> Dihydropyrimidinase related protein-2
<222> (1)..(572)
<223> Accession No. as of 29 August 2003: Q16555
<400> 95

Met Ser Tyr Gln Gly Lys Lys Asn Ile Pro Arg Ile Thr Ser Asp Arg
1   5   10   15

Leu Leu Ile Lys Gly Gly Lys Ile Val Asn Asp Asp Gln Ser Phe Tyr
            20   25   30

Ala Asp Ile Tyr Met Glu Asp Gly Leu Ile Lys Gln Ile Gly Glu Asn
        35   40   45

Leu Ile Val Pro Gly Gly Val Lys Thr Ile Glu Ala His Ser Arg Met
    50   55   60

Val Ile Pro Gly Gly Ile Asp Val His Thr Arg Phe Gln Met Pro Asp
65   70   75   80

Gln Gly Met Thr Ser Ala Asp Asp Phe Phe Gln Gly Thr Lys Ala Ala
                85   90   95

Leu Ala Gly Gly Thr Thr Met Ile Ile Asp His Val Val Pro Glu Pro
                100   105   110

Gly Thr Ser Leu Leu Ala Ala Phe Asp Gln Trp Arg Glu Trp Ala Asp
5   115   120   125

Ser Lys Ser Cys Cys Asp Tyr Ser Leu His Val Asp Ile Ser Glu Trp
            130   135   140

His Lys Gly Ile Gln Glu Glu Met Glu Ala Leu Val Lys Asp His Gly
10 145   150   155   160

Val Asn Ser Phe Leu Val Tyr Met Ala Phe Lys Asp Arg Phe Gln Leu
                165   170   175

Thr Asp Cys Gln Ile Tyr Glu Val Leu Ser Val Ile Arg Asp Ile Gly
                180   185   190

Ala Ile Ala Gln Val His Ala Glu Asn Gly Asp Ile Ile Ala Glu Glu
15   195   200   205

Gln Gln Arg Ile Leu Asp Leu Gly Ile Thr Gly Pro Glu Gly His Val
                210   215   220

Leu Ser Arg Pro Glu Glu Val Glu Ala Glu Ala Val Asn Arg Ala Ile
20 225   230   235   240

Thr Ile Ala Asn Gln Thr Asn Cys Pro Leu Tyr Ile Thr Lys Val Met
                245   250   255

Ser Lys Ser Ser Ala Glu Val Ile Ala Gln Ala Arg Lys Gly Thr
                260   265   270

Val Val Tyr Gly Glu Pro Ile Thr Ala Ser Leu Gly Thr Asp Gly Ser
275   280   285

His Tyr Trp Ser Lys Asn Trp Ala Lys Ala Ala Phe Val Thr Ser
290   295   300

5   Pro Pro Leu Ser Pro Asp Pro Thr Thr Pro Asp Phe Leu Asn Ser Leu
305   310   315   320

Leu Ser Cys Gly Asp Leu Gln Val Thr Gly Ser Ala His Cys Thr Phe
325   330   335

Asn Thr Ala Gln Lys Ala Val Gly Lys Asp Asn Phe Thr Leu Ile Pro
10   340   345   350

Glu Gly Thr Asn Gly Thr Glu Glu Arg Met Ser Val Ile Trp Asp Lys
355   360   365

Ala Val Val Thr Gly Lys Met Asp Glu Asn Gln Phe Val Ala Val Thr
370   375   380

15 Ser Thr Asn Ala Ala Lys Val Phe Asn Leu Tyr Pro Arg Lys Gly Arg
385   390   395   400

Ile Ala Val Gly Ser Asp Ala Asp Leu Val Ile Trp Asp Pro Asp Ser
405   410   415

Val Lys Thr Ile Ser Ala Lys Thr His Asn Ser Ser Leu Glu Tyr Asn
20   420   425   430

Ile Phe Glu Gly Met Glu Cys Arg Gly Ser Pro Leu Val Val Ile Ser
435   440   445

Gln Gly Lys Ile Val Leu Glu Asp Gly Thr Leu His Val Thr Glu Gly
450   455   460

Ser Gly Arg Tyr Ile Pro Arg Lys Pro Phe Pro Asp Phe Val Tyr Lys
465   470   475   480

Arg Ile Lys Ala Arg Ser Arg Leu Ala Glu Leu Arg Gly Val Pro Arg
485   490   495

5   Gly Leu Tyr Asp Gly Pro Val Cys Glu Val Ser Val Thr Pro Lys Thr
500   505   510

Val Thr Pro Ala Ser Ser Ala Lys Thr Ser Pro Ala Lys Gln Gln Ala
515   520   525

Pro Pro Val Arg Asn Leu His Gln Ser Gly Phe Ser Leu Ser Gly Ala
10   530   535   540

Gln Ile Asp Asp Asn Ile Pro Arg Arg Thr Thr Gln Arg Ile Val Ala
545   550   555   560

Pro Pro Gly Gly Arg Ala Asn Ile Thr Ser Leu Gly
565   570

15

<210> 96
<211> 500
<212> PRT
<213> Homo sapiens
20 <220>
<221> 4-aminobutyrate aminotransferase, mitochondrial precursor
<222> (1)..(500)
<223> Accession No. as of 29 August 2003: P80404

<400> 96

```
Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His
1               5                   10                  15

Thr Tyr Arg Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala
            20                  25                  30

Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met Lys Thr
    35                  40                  45

Glu Val Pro Gly Pro Arg Ser Gln Glu Leu Met Lys Gln Leu Asn Ile
10  50                  55                  60

Ile Gln Asn Ala Glu Ala Val His Phe Cys Asn Tyr Glu Glu Ser
        65                  70                  75              80

Arg Gly Asn Tyr Leu Val Asp Val Asp Gly Asn Arg Met Leu Asp Leu
            85                  90                  95

Tyr Ser Gln Ile Ser Ser Val Pro Ile Gly Tyr Ser Asp Pro Ala Leu
15      100                 105                 110

Val Lys Leu Ile Gln Gln Pro Gln Asn Ala Ser Met Phe Val Asn Arg
        115                 120                 125

Pro Ala Leu Glu Ile Leu Pro Pro Glu Asn Phe Val Glu Lys Leu Arg
        130                 135                 140

Gln Ser Leu Leu Ser Val Ala Pro Lys Gly Met Ser Gln Leu Ile Thr
20      145                 150                 155             160

Met Ala Cys Gly Ser Cys Ser Asn Glu Asn Ala Leu Lys Thr Ile Phe
        165                 170                 175
```

```
Met Trp Tyr Arg Ser Lys Glu Arg Arg Gly Gln Arg Gly Phe Ser Lys Glu
                180                 185                 190

Glu Leu Glu Cys Met Ile Asn Gln Ala Pro Trp Cys Pro Asp Tyr
            195                 200                 205

Ser Ile Leu Ser Phe Met Gly Ser Phe His Gly Arg Thr Met Gly Cys
5       210                 215                 220

Leu Ala Thr Thr His Ser Lys Ala Ile His Lys Ile Asp Ile Pro Ser
    225                 230                 235             240

Phe Asp Trp Pro Ile Ala Pro Phe Pro Arg Leu Lys Tyr Pro Leu Glu
10      245                 250                 255

Glu Phe Val Lys Glu Asn Gln Gln Glu Glu Ala Gly Leu Glu Glu
        260                 265                 270

Val Glu Asp Leu Ile Val Lys Tyr Arg Lys Lys Lys Thr Val Ala
    275                 280                 285

Gly Ile Ile Val Glu Pro Ile Gln Ser Glu Gly Gly Asp Asn His Ala
15      290                 295                 300

Ser Asp Asp Phe Phe Arg Lys Leu Arg Asp Ile Ala Arg Lys His Cys
        305                 310                 315             320

Cys Ala Phe Leu Val Asp Glu Val Gln Thr Gly Gly Gly Cys Thr Gly
20      325                 330                 335

Lys Phe Trp Ala His Glu His Trp Gly Leu Asp Asp Pro Ala Asp Val
        340                 345                 350

Met Thr Phe Ser Lys Met Met Thr Gly Gly Phe Phe Leu Lys Glu
        355                 360                 365
```

```
Glu Phe Arg Pro Asn Ala Pro Tyr Arg Ile Phe Asn Thr Trp Leu Gly
            370                 375                 380

Asp Pro Ser Lys Asn Leu Leu Ala Glu Val Ile Asn Ile Ile Lys
385                 390                 395                 400

5   Arg Glu Asp Leu Leu Asn Asn Ala Ala His Ala Gly Lys Ala Leu Leu
                        405                 410                 415

    Thr Gly Leu Leu Asp Leu Gln Ala Arg Tyr Pro Gln Phe Ile Ser Arg
                        420                 425                 430

    Val Arg Gly Arg Gly Thr Phe Cys Ser Phe Asp Thr Pro Asp Asp Ser
10                      435                 440                 445

    Ile Arg Asn Lys Leu Ile Leu Ala Arg Asn Lys Gly Val Val Leu
                450                 455                 460

    Gly Gly Cys Gly Asp Lys Ser Ile Arg Phe Arg Pro Thr Leu Val Phe
    465                 470                 475                 480

15  Arg Asp His His Ala His Leu Phe Leu Asn Ile Phe Ser Asp Ile Leu
                        485                 490                 495

    Ala Asp Phe Lys
    500
```

<210> 97

<211> 423

<212> PRT

<213> Homo sapiens

<220>

<221> Glycine amidiontransferase, mitochondrial precursor

<222> (1)..(423)

<223> Accession No. as of 29 August 2003: P50440

5   <400> 97

```
Met Leu Arg Val Arg Cys Leu Arg Gly Gly Ser Arg Gly Ala Glu Ala
1                   5                   10                  15

Val His Tyr Ile Gly Ser Arg Leu Gly Arg Thr Leu Thr Gly Trp Val
                20                  25                  30

Gln Arg Thr Phe Gln Ser Thr Gln Ala Ala Thr Ala Ser Ser Arg Asn
            35                  40                  45

Ser Cys Ala Ala Asp Asp Lys Ala Thr Glu Pro Leu Pro Lys Asp Cys
    50                  55                  60

Pro Val Ser Ser Tyr Asn Glu Trp Asp Pro Leu Glu Glu Val Ile Val
15  65                  70                  75                  80

Gly Arg Ala Glu Asn Ala Cys Val Pro Pro Phe Thr Ile Glu Val Lys
                85                  90                  95

Ala Asn Thr Tyr Glu Lys Tyr Trp Pro Phe Tyr Gln Lys Gln Gly Gly
            100                 105                 110

His Tyr Phe Pro Lys Asp His Leu Lys Lys Ala Val Ala Glu Ile Glu
20  115                 120                 125

Glu Met Cys Asn Ile Leu Lys Thr Glu Gly Val Thr Val Arg Arg Pro
    130                 135                 140
```

Asp Pro Ile Asp Trp Ser Lys Tyr Lys Thr Pro Asp Phe Glu Ser
145   150   155   160

Thr Gly Leu Tyr Ser Ala Met Pro Arg Asp Ile Leu Ile Val Val Gly
            165   170   175

5   Asn Glu Ile Glu Ile Glu Ala Pro Met Ala Trp Arg Ser Arg Phe Phe Glu
            180   185   190

Tyr Arg Ala Tyr Arg Ser Ile Ile Lys Asp Tyr Phe His Arg Gly Ala
            195   200   205

Lys Trp Thr Thr Ala Pro Lys Pro Thr Met Ala Asp Glu Leu Tyr Asn
10 210   215   220

Gln Asp Tyr Pro Ile His Ser Val Glu Asp Arg His Lys Leu Ala Ala
225   230   235   240

Gln Gly Lys Phe Val Thr Thr Glu Phe Glu Pro Cys Phe Asp Ala Ala
            245   250   255

15 Asp Phe Ile Arg Ala Gly Arg Asp Ile Phe Ala Gln Arg Ser Gln Val
            260   265   270

Thr Asn Tyr Leu Gly Ile Glu Trp Met Arg Arg His Leu Ala Pro Asp
            275   280   285

Tyr Arg Val His Ile Ile Ser Phe Lys Asp Pro Asn Pro Met His Ile
20 290   295   300

Asp Ala Thr Phe Asn Ile Ile Gly Pro Gly Ile Val Leu Ser Asn Pro
305   310   315   320

Asp Arg Pro Cys His Gln Ile Asp Leu Phe Lys Lys Ala Gly Trp Thr
            325   330   335

Ile Ile Thr Pro Pro Thr Pro Ile Ile Pro Asp Asp His Pro Leu Trp
            340   345   350

Met Ser Ser Lys Trp Leu Ser Met Asn Val Leu Met Leu Asp Glu Lys
            355   360   365

5   Arg Val Met Val Asp Ala Asn Glu Val Pro Ile Gln Lys Met Phe Glu
            370   375   380

Lys Leu Gly Ile Thr Thr Ile Lys Val Asn Ile Arg Asn Ala Asn Ser
385   390   395   400

Leu Gly Gly Gly Phe His Cys Trp Thr Cys Asp Val Arg Arg Arg Gly
10   405   410   415

Thr Leu Gln Ser Tyr Leu Asp
            420

15 <210> 98

<211> 654

<212> PRT

<213> Homo sapiens

<220>

20 <221> GRP 78

<222> (1)..(654)

<223> Accession No. as of 29 August 2003: P11021

<220>

<221> misc_feature

<222> (302)..(302)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (329)..(329)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (344)..(344)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (461)..(461)

<223> Xaa can be any naturally occurring amino acid

<400> 98

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Met Lys Leu Ser Leu Val Ala Ala Met Leu Leu Leu Leu Ser Ala
1               5                   10                  15

Ala Arg Ala Lys Glu Glu Asp Met Gly Thr Val Val Ala Ile His Leu
            20                  25                  30

Gly Thr Tyr Pro Cys Val Gly Val Phe Lys Asn Gly Arg Met Glu
        35                  40                  45

Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Met Pro Ser Tyr Val Ala
    50                  55                  60
```

```
Phe Thr Pro Glu Gly Glu Cys Leu Ile Gly Asp Ala Ala Lys Asn Gln
                65                  70                  75              80

Leu Thr Ser Asn Pro Lys Asn Thr Val Phe Asp Ala Lys Arg Leu Ile
                85                  90                  95

Gly Arg Arg Trp His Asp Pro Ser Val Gln Gln Asp Ile Glu Phe Leu
5               100                 105                 110

Pro Phe Lys Val Val Glu Lys Asn Thr Lys Ser Tyr Ile Gln Ile Asp
                115                 120                 125

Val Gly Gly Gln Thr Lys Thr Phe Ala Pro Lys Glu Ile Ser Ala
10              130                 135                 140

Met Val Leu Thr Lys Met Glu Asn Ala Glu Tyr Leu Gly Lys
                145                 150                 155             160

Val Thr His Ala Val Val Thr Ala Pro Ala Tyr Phe Asn Asp Ala Gln
                165                 170                 175

Cys Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Asp Leu Asn Val Met
15              180                 185                 190

Arg Ile Asn Lys Pro Thr Ala Ala Ile Ala Tyr Gly Leu Asp
                195                 200                 205

Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly Gly Gly
20              210                 215                 220

Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe Lys Val
                225                 230                 235             240

Val Ala Thr Asn Gly Asp Thr Tyr Leu Gly Gly Glu Asp Phe Asp Gln
                245                 250                 255
```

```
Arg Val Met Glu His Ile Phe Ile Lys Leu Tyr Lys Lys Thr Gly Lys
        260            265            270
Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Trp Arg Lys Val
        275            280            285
Glu Lys Ala Lys Arg Ala Leu Ser Gln His Gln Ala Xaa Val Ile
5       290            295            300
Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu Thr
        305            310            315            320
Gln Ala Lys Phe Glu Glu Leu Asn Xaa Asp Leu Phe Gln Ser Thr Met
10      325            330            335
Lys Pro Ser Gln Arg Ser Val Xaa Lys Val Leu Glu Asp Ser Asp Leu
        340            345            350
Lys Lys Ser Asp Ile Asp Glu Thr Val Leu Val Gly Gly Phe Thr Gln
        355            360            365
Ile Pro Lys Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu
15      370            375            380
Leu Ser Arg Gly Ile Ser Pro Tyr Glu Ala Val Ala Tyr Gly Ala Ala
        385            390            395            400
Val Gln Ala Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val
        405            410            415
Leu Leu Asp Ile Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly
20      420            425            430
Val Met Thr Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys
        435            440            445
```

```
Ser Gln Ile Phe Ser Thr Ala Phe Asp Asn Gln Pro Xaa Thr Ile Lys
        450            455            460
Val Tyr Glu Gly Lys Gln Pro Leu Thr Lys Asp Asn His Leu Leu Gly
        465            470            475            480
Thr Phe Asp Leu Thr Gly Ile Pro Pro Ala Pro Cys Gly Val Pro Gln
5       485            490            495
Ile Glu Val Thr Phe Glu Met Asp Val Ser Asp Ile Leu Gln Val Thr
        500            505            510
Ala Lys Asp Lys Gly Thr Arg Tyr Lys Asn Lys Ile Thr Ile Thr Asn
10      515            520            525
Asp Gln Asn His Leu Thr Pro Glu Asp Ile Glu Arg Met Val Asn Asp
        530            535            540
Ala Glu Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Cys Thr Asp
        545            550            555            560
Thr Arg Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile
15      565            570            575
Gly Asp Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu
        580            585            590
Thr Met Glu Lys Thr Val Glu Glu Lys Thr Trp Leu Glu Ser His
20      595            600            605
Gln Asp Ala Asp Thr Glu Asp Phe Lys Ala Lys Lys Glu Leu Glu
        610            615            620
Glu Ile Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro
        625            630            635            640
```

Pro Pro Thr Gly Glu Asp Thr Ala Glu Lys Asp Glu Leu
             645   650

5 <210> 99

   <211> 325

   <212> PRT

   <213> Homo sapiens

   <220>

10 <221> Eukaryotic translation initiation factor 3 subunit 2

   <222> (1)..(325)

   <223> Accession No. as of 29 August 2003: Q13347

   <400> 99

15 Met Lys Pro Ile Leu Leu Gln Gly His Glu Arg Ser Ile Thr Gln Ile
   1   5   10   15

   Lys Tyr Asn Arg Glu Gly Asp Leu Leu Phe Thr Val Ala Lys Asp Pro
               20   25   30

   Ile Val Asn Val Trp Tyr Ser Val Asn Gly Glu Arg Leu Gly Thr Tyr
20   35   40   45

   Met Gly His Thr Gly Ala Val Trp Cys Val Asp Ala Asp Trp Asp Thr
               50   55   60

   Lys His Val Leu Thr Gly Ser Ala Asp Asn Ser Cys Arg Leu Trp Asp
   65   70   75   80

   Cys Glu Thr Gly Lys Gln Leu Ala Leu Leu Lys Thr Asn Ser Ala Val
               85   90   95

   Arg Thr Cys Gly Phe Asp Phe Gly Gly Asn Ile Ile Met Phe Ser Thr
               100   105   110

5 Asp Lys Gln Met Gly Tyr Gln Cys Phe Val Ser Phe Phe Asp Leu Arg
               115   120   125

   Asp Pro Ser Gln Ile Asp Asn Glu Tyr Met Lys Ile Pro Cys
               130   135   140

   Asn Asp Ser Lys Ile Thr Ser Ala Val Trp Gly Pro Leu Gly Glu Cys
10 145   150   155   160

   Ile Ile Ala Gly His Glu Ser Gly Glu Leu Asn Gln Tyr Ser Ala Lys
               165   170   175

   Ser Gly Glu Val Leu Val Asn Val Lys Glu His Ser Arg Gln Ile Asn
               180   185   190

15 Asp Ile Gln Leu Ser Arg Asp Met Thr Met Phe Val Thr Ala Ser Lys
               195   200   205

   Asp Asn Thr Ala Lys Leu Phe Asp Ser Thr Thr Leu Glu His Gln Lys
               210   215   220

   Thr Phe Arg Thr Glu Arg Pro Val Asn Ser Ala Ala Leu Ser Pro Asn
20 225   230   235   240

   Tyr Asp His Val Val Leu Gly Gly Gly Gln Glu Ala Met Asp Val Thr
               245   250   255

   Thr Thr Ser Thr Arg Ile Gly Lys Phe Glu Ala Arg Phe Phe His Leu
               260   265   270

Ala Phe Glu Glu Phe Arg Val Lys Gly His Phe Gly Pro Ile
                    275   280   285

Asn Ser Val Ala Phe His Pro Asp Gly Lys Ser Tyr Ser Ser Gly Gly
            290   295   300

5   Glu Asp Gly Tyr Val Arg Ile His Tyr Phe Asp Pro Gln Tyr Phe Glu
            305   310   315   320

    Phe Glu Phe Glu Ala
                    325

10

    <210> 100
    <211> 572
    <212> PRT
    <213> Homo sapiens
    <220>
15 <221> Dihydropyrimidinase related protein-2
    <222> (1)..(572)
    <223> Accession No. as of 29 August 2003: Q16555
    <400> 100

20

    Met Ser Tyr Gln Gly Lys Lys Asn Ile Pro Arg Ile Thr Ser Asp Arg
    1   5   10   15

    Leu Leu Ile Lys Gly Gly Lys Ile Val Asn Asp Asp Gln Ser Phe Tyr
            20   25   30

Ala Asp Ile Tyr Met Glu Asp Gly Leu Ile Lys Gln Ile Gly Glu Asn
            35   40   45

Leu Ile Val Pro Gly Gly Val Lys Thr Ile Glu Ala His Ser Ser Arg Met
            50   55   60

5   Val Ile Pro Gly Gly Ile Asp Val His Thr Arg Phe Gln Met Pro Asp
            65   70   75   80

    Gln Gly Met Thr Ser Ala Asp Asp Phe Phe Gln Gly Thr Lys Ala Ala
            85   90   95

    Leu Ala Gly Gly Thr Thr Met Ile Ile Asp His Val Val Pro Glu Pro
10   100   105   110

    Gly Thr Ser Leu Leu Ala Ala Phe Asp Gln Trp Arg Glu Trp Ala Asp
            115   120   125

    Ser Lys Ser Cys Cys Asp Tyr Ser Leu His Val Asp Ile Ser Glu Trp
            130   135   140

15 His Lys Gly Ile Gln Glu Glu Met Glu Ala Leu Val Lys Asp His Gly
            145   150   155   160

    Val Asn Ser Phe Leu Val Tyr Met Ala Phe Lys Asp Arg Phe Gln Leu
            165   170   175

    Thr Asp Cys Gln Ile Tyr Glu Val Leu Ser Val Ile Arg Asp Ile Gly
20   180   185   190

    Ala Ile Ala Gln Val His Ala Glu Asn Gly Asp Ile Ile Ala Glu Glu
            195   200   205

    Gln Gln Arg Ile Leu Asp Leu Gly Ile Thr Gly Pro Glu Gly His Val
            210   215   220

```
   Leu Ser Arg Pro Glu Glu Val Ala Glu Ala Val Asn Arg Ala Ile
                225            230            235            240

   Thr Ile Ala Asn Gln Thr Asn Cys Pro Leu Tyr Ile Thr Lys Val Met
                245            250            255

 5 Ser Lys Ser Ser Ala Glu Val Ile Ala Gln Ala Arg Lys Lys Gly Thr
                260            265            270

   Val Val Tyr Gly Glu Pro Ile Thr Ala Ser Leu Gly Thr Asp Gly Ser
                275            280            285

10 His Tyr Trp Ser Lys Asn Trp Ala Lys Ala Ala Ala Phe Val Thr Ser
                290            295            300

   Pro Pro Leu Ser Pro Asp Pro Thr Thr Pro Asp Phe Leu Asn Ser Leu
                305            310            315            320

   Leu Ser Cys Gly Asp Leu Gln Val Thr Gly Ser Ala His Cys Thr Phe
                325            330            335

15 Asn Thr Ala Gln Lys Ala Val Gly Lys Asp Asn Phe Thr Leu Ile Pro
                340            345            350

   Glu Gly Thr Asn Gly Thr Glu Glu Arg Met Ser Val Ile Trp Asp Lys
                355            360            365

   Ala Val Val Thr Gly Lys Met Asp Glu Asn Gln Phe Val Ala Val Thr
                370            375            380

20 Ser Thr Asn Ala Ala Lys Val Phe Asn Leu Tyr Pro Arg Lys Gly Arg
                385            390            395            400

   Ile Ala Val Gly Ser Asp Ala Asp Leu Val Ile Trp Asp Pro Asp Ser
                405            410            415
```

```
   Val Lys Thr Ile Ser Ala Lys Thr His Asn Ser Leu Glu Tyr Asn
                420            425            430

   Ile Phe Glu Gly Met Glu Cys Arg Gly Ser Leu Val Val Ile Ser
                435            440            445

 5 Gln Gly Lys Ile Val Leu Glu Asp Gly Thr Leu His Val Thr Glu Gly
                450            455            460

   Ser Gly Arg Tyr Ile Pro Arg Lys Pro Asp Phe Val Tyr Lys
                465            470            475            480

   Arg Ile Lys Ala Arg Ser Arg Leu Ala Glu Leu Arg Gly Val Pro Arg
                485            490            495

10 Gly Leu Tyr Asp Gly Pro Val Cys Glu Val Ser Val Thr Pro Lys Thr
                500            505            510

   Val Thr Pro Ala Ser Ser Ala Lys Thr Ser Pro Ala Lys Gln Gln Ala
                515            520            525

15 Pro Pro Val Arg Asn Leu His Gln Ser Gly Phe Ser Leu Ser Gly Ala
                530            535            540

   Gln Ile Asp Asp Asn Ile Pro Arg Arg Thr Gln Arg Ile Val Ala
                545            550            555            560

   Pro Pro Gly Gly Arg Ala Asn Ile Thr Ser Leu Gly
20              565            570


   <210>  101

   <211>  561
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<212> PRT

<213> Homo sapiens

<220>

<221> Phosphoglucomutase (EC 5.4.2.2) (Glucose phosphomutase) (PGM)

5 <222> (1)..(561)

<223> Accession No. as of 29 August 2003: P36871

<400> 101

Val Lys Ile Val Thr Val Lys Thr Gln Ala Tyr Gln Asp Gln Lys Pro
10 1   5   10   15

Gly Thr Ser Gly Leu Arg Lys Arg Val Lys Val Phe Gln Ser Ser Ala
                20   25   30

Asn Tyr Ala Glu Asn Phe Ile Gln Ser Ile Ile Ser Thr Val Glu Pro
            35   40   45

Ala Gln Arg Gln Glu Ala Thr Leu Val Val Gly Gly Asp Gly Arg Phe
15   50   55   60

Tyr Met Lys Glu Ala Ile Gln Leu Ile Ala Arg Ile Ala Ala Ala Asn
65   70   75   80

Gly Ile Gly Arg Leu Val Ile Gly Gln Asn Gly Ile Leu Ser Thr Pro
                85   90   95

Ala Val Ser Cys Ile Ile Arg Lys Ile Lys Ala Ile Gly Gly Ile Ile
20   100   105   110

Leu Thr Ala Ser His Asn Pro Gly Gly Pro Asn Gly Asp Phe Gly Ile
                115   120   125

Lys Phe Asn Ile Ser Asn Gly Gly Pro Ala Pro Glu Ala Ile Thr Asp
                130   135   140

Lys Ile Phe Gln Ile Ser Lys Thr Glu Glu Tyr Ala Ala Val Cys Pro
145   150   155   160

5 Asp Leu Lys Val Asp Leu Gly Val Leu Gly Lys Gln Gln Phe Asp Leu
                165   170   175

Glu Asn Lys Phe Lys Pro Phe Thr Val Glu Ile Val Asp Ser Val Glu
                180   185   190

Ala Tyr Ala Thr Met Leu Arg Ser Ile Phe Asp Phe Ser Ala Leu Lys
10   195   200   205

Glu Leu Leu Ser Gly Pro Asn Arg Leu Lys Ile Arg Ile Asp Ala Met
                210   215   220

His Gly Val Val Gly Pro Tyr Val Lys Lys Ile Leu Cys Glu Glu Leu
225   230   235   240

Gly Ala Pro Ala Asn Ser Ala Val Asn Cys Val Pro Leu Glu Asp Phe
15   245   250   255

Gly Gly His His Pro Asp Pro Asn Leu Thr Tyr Ala Ala Asp Leu Val
                260   265   270

Glu Thr Met Lys Ser Gly Glu His Asp Phe Gly Ala Ala Phe Asp Gly
20   275   280   285

Asp Gly Asp Arg Asn Met Ile Leu Gly Lys His Gly Phe Phe Val Asn
                290   295   300

Pro Ser Asp Ser Val Ala Val Ile Ala Ala Asn Ile Phe Ser Ile Pro
305   310   315   320

Tyr Phe Gln Gln Thr Gly Val Arg Gly Phe Ala Arg Ser Met Pro Thr
325   330   335

Ser Gly Ala Leu Asp Arg Val Ala Ser Ala Thr Lys Ile Ala Leu Tyr
340   345   350

5   Glu Thr Pro Thr Gly Trp Lys Phe Phe Gly Asn Leu Met Asp Ala Ser
355   360   365

Lys Leu Ser Leu Cys Gly Glu Ser Phe Gly Thr Gly Ser Asp His
370   375   380

Ile Arg Glu Lys Asp Gly Leu Trp Ala Val Leu Ala Trp Leu Ser Ile
10 385   390   395   400

Leu Ala Thr Arg Lys Gln Ser Val Glu Asp Ile Leu Lys Asp His Trp
405   410   415

Gln Lys Tyr Gly Arg Asn Phe Phe Thr Arg Tyr Asp Tyr Glu Glu Val
420   425   430

15 Glu Ala Glu Gly Ala Asn Lys Met Met Lys Asp Leu Glu Ala Leu Met
435   440   445

Phe Asp Arg Ser Phe Val Gly Lys Gln Phe Ser Ala Asn Asp Lys Val
450   455   460

Tyr Thr Val Glu Lys Ala Asp Asn Phe Glu Tyr Ser Asp Pro Val Asp
465   470   475   480

20 465   Gly Ser Ile Ser Arg Asn Gln Gly Leu Arg Leu Ile Phe Thr Asp Gly
485   490   495

Ser Arg Ile Val Phe Arg Leu Ser Gly Thr Gly Ser Ala Gly Ala Thr
500   505   510

Ile Arg Leu Tyr Ile Asp Ser Tyr Glu Lys Asp Val Ala Lys Ile Asn
515   520   525

Gln Asp Pro Gln Val Met Leu Ala Pro Leu Ile Ser Ala Leu Lys
530   535   540

5   Val Ser Gln Leu Gln Glu Arg Gly Arg Thr Ala Pro Thr Val Ile
545   550   555   560

Thr

10

<210> 102
<211> 263
<212> PRT
<213> Homo sapiens

15 <220>
<221> Proteasome subunit alpha type 1
<222> (1)..(263)
<223> Accession No. as of 29 August 2003: P25786

<400> 102

20

Met Phe Arg Asn Gln Tyr Asp Asn Asp Val Thr Val Trp Ser Pro Gln
1   5   10   15

Gly Arg Ile His Gln Ile Glu Tyr Ala Met Glu Ala Val Lys Gln Gly
20   25   30

Ser Ala Thr Val Gly Leu Lys Ser Lys Thr His Ala Val Leu Val Ala
                35   40   45

Leu Lys Arg Ala Gln Ser Glu Leu Ala Ala His Gln Lys Lys Ile Leu
          50   55   60

5   His Val Asp Asn His Ile Gly Ile Ser Ile Ala Gly Leu Thr Ala Asp
                65   70   75   80

Ala Arg Leu Leu Cys Asn Phe Met Arg Gln Glu Cys Leu Asp Ser Arg
                      85   90   95

Phe Val Phe Asp Arg Pro Leu Pro Val Ser Arg Leu Val Ser Leu Ile
10   100   105   110

Gly Ser Lys Thr Gln Ile Pro Thr Gln Arg Tyr Gly Arg Arg Pro Tyr
              115   120   125

Gly Val Gly Leu Leu Ile Ala Gly Tyr Asp Asp Met Gly Pro His Ile
              130   135   140

15 Phe Gln Thr Cys Pro Ser Ala Asn Tyr Phe Asp Cys Arg Ala Met Ser
              145   150   155   160

Ile Gly Ala Arg Ser Gln Ser Ala Arg Thr Tyr Leu Glu Arg His Met
              165   170   175

Ser Glu Phe Met Glu Cys Asn Leu Asn Glu Leu Val Lys His Gly Leu
              180   185   190

20 Arg Ala Leu Arg Glu Thr Leu Pro Ala Glu Gln Asp Leu Thr Thr Lys
              195   200   205

Asn Val Ser Ile Gly Ile Val Gly Lys Asp Leu Glu Phe Ile Thr Tyr
              210   215   220

Asp Asp Asp Val Ser Pro Phe Leu Glu Gly Leu Glu Glu Arg Pro
              225   230   235   240

Gln Arg Lys Ala Gln Pro Ala Gln Pro Ala Asp Glu Pro Ala Glu Lys
                      245   250   255

5   Ala Asp Glu Pro Met Glu His
                      260

<210> 103
<211> 205
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<212> PRT
<213> Homo sapiens
<220>
<221> Heat shock 27 kDa protein
15 <222> (1)..(205)
<223> Accession No. as of 29 August 2003: P04792
<400> 103

Met Thr Glu Arg Arg Val Pro Phe Ser Leu Arg Gly Pro Ser Trp
20 1   5   10   15

Asp Pro Phe Arg Asp Trp Tyr Pro His Ser Arg Leu Phe Asp Gln Ala
                      20   25   30

Phe Gly Leu Pro Arg Leu Pro Glu Glu Trp Ser Gln Trp Leu Gly Gly
              35   40   45

```
    Ser Ser Trp Pro Gly Tyr Val Arg Pro Leu Pro Pro Ala Ala Ile Glu
                50                  55                  60

    Ser Pro Ala Val Ala Pro Ala Tyr Ser Arg Ala Leu Ser Arg Gln
            65                  70                  75                  80

5   Leu Ser Ser Gly Val Ser Glu Ile Arg His Thr Ala Asp Arg Trp Arg
                85                  90                  95

    Val Ser Leu Asp Val Asn His Phe Ala Pro Asp Glu Leu Thr Val Lys
                    100                 105                 110

    Thr Lys Asp Gly Val Val Ile Glu Thr Gly Lys His Glu Glu Arg Gln
10  115                 120                 125

    Asp Glu His Gly Tyr Ile Ser Arg Cys Phe Thr Arg Lys Tyr Thr Leu
                130                 135                 140

    Pro Pro Gly Val Asp Pro Thr Gln Val Ser Ser Ser Leu Ser Pro Glu
15  145                 150                 155                 160

    Gly Thr Leu Thr Val Glu Ala Pro Met Pro Lys Leu Ala Thr Gln Ser
                165                 170                 175

    Asn Glu Ile Thr Ile Pro Val Thr Phe Glu Ser Arg Ala Gln Leu Gly
                180                 185                 190

    Gly Pro Glu Ala Ala Lys Ser Asp Glu Thr Ala Ala Lys
20  195                 200                 205
```

<210> 104
<211> 868

<212> PRT

<213> Homo sapiens

<220>

<221> Programmed cell death 6 interacting protein (Hp95)

5   <222> (1)..(868)

<223> Accession No. as of 29 August 2003: Q8WUM4

<400> 104

```
    Met Ala Thr Phe Ile Ser Val Gln Leu Lys Lys Thr Ser Glu Val Asp
10  1                5                   10                  15

    Leu Ala Lys Pro Leu Val Lys Phe Ile Gln Gln Thr Tyr Pro Ser Gly
                20                  25                  30

    Gly Glu Glu Gln Ala Gln Tyr Cys Arg Ala Ala Glu Glu Leu Ser Lys
15  35                  40                  45

    Leu Arg Arg Ala Ala Val Gly Arg Pro Leu Asp Lys His Glu Gly Ala
            50                  55                  60

    Leu Glu Thr Leu Leu Arg Tyr Tyr Asp Gln Ile Cys Ser Ile Glu Pro
            65                  70                  75                  80

    Lys Phe Pro Phe Ser Glu Asn Gln Ile Cys Leu Thr Phe Thr Trp Lys
20  85                  90                  95

    Asp Ala Phe Asp Lys Gly Ser Leu Phe Gly Gly Ser Val Lys Leu Ala
                    100                 105                 110

    Leu Ala Ser Leu Gly Tyr Glu Lys Ser Cys Val Leu Phe Asn Cys Ala
            115                 120                 125
```

Ala Leu Ala Ser Gln Ile Ala Ala Glu Gln Asn Leu Asp Asn Asp Glu
130   135   140

Gly Leu Lys Ile Ala Ala Lys His Tyr Gln Phe Ala Ser Gly Ala Phe
145   150   155   160

Leu His Ile Lys Glu Thr Val Leu Ser Ala Leu Ser Arg Glu Pro Thr
5 165   170   175

Val Asp Ile Ser Pro Asp Thr Val Gly Thr Leu Ser Leu Ile Met Leu
180   185   190

Ala Gln Ala Gln Glu Val Phe Phe Leu Lys Ala Thr Arg Asp Lys Met
10 195   200   205

Lys Asp Ala Ile Ile Lys Leu Ala Asn Gln Ala Ala Asp Tyr Phe
210   215   220

Gly Asp Ala Phe Lys Gln Cys Gln Tyr Lys Asp Thr Leu Pro Lys Glu
225   230   235   240

Val Phe Pro Val Leu Ala Ala Lys His Cys Ile Met Gln Ala Asn Ala
15 245   250   255

Glu Tyr His Gln Ser Ile Leu Ala Lys Gln Gln Lys Lys Phe Gly Glu
260   265   270

Glu Ile Ala Arg Leu Gln His Ala Ala Glu Leu Ile Lys Thr Val Ala
275   280   285

Ser Arg Tyr Asp Glu Tyr Val Asn Val Lys Asp Phe Ser Asp Lys Ile
20 290   295   300

Asn Arg Ala Leu Ala Ala Lys Lys Asp Asn Asp Phe Ile Tyr His
305   310   315   320

Asp Arg Val Pro Asp Leu Lys Asp Leu Asp Pro Ile Gly Lys Ala Thr
325   330   335

Leu Val Lys Ser Thr Pro Val Asn Val Pro Ile Ser Gln Lys Phe Thr
340   345   350

Asp Leu Phe Glu Lys Met Val Pro Val Ser Val Gln Gln Ser Leu Ala
5 355   360   365

Ala Tyr Asn Gln Arg Lys Ala Leu Asp Val Asn Arg Ser Ile Ala Gln
370   375   380

Met Arg Glu Ala Thr Thr Leu Ala Asn Gly Val Leu Ala Ser Leu Asn
10 385   390   395   400

Leu Pro Ala Ala Ile Glu Asp Val Ser Gly Asp Thr Val Pro Gln Ser
405   410   415

Ile Leu Thr Lys Ser Arg Ser Val Ile Glu Gln Gly Gly Ile Gln Thr
420   425   430

Val Asp Gln Leu Ile Lys Glu Leu Pro Glu Leu Leu Gln Arg Asn Arg
15 435   440   445

Glu Ile Leu Asp Glu Ser Leu Arg Leu Leu Asp Glu Glu Ala Thr
450   455   460

Asp Asn Asp Leu Arg Ala Ala Phe Lys Glu Lys Arg Trp Gln Arg Thr Pro
20 465   470   475   480

Ser Asn Glu Leu Tyr Pro Leu Arg Ala Glu Gly Thr Asn Phe Arg
485   490   495

Thr Val Leu Asp Lys Ala Val Gln Ala Asp Gly Gln Val Lys Glu Cys
500   505   510

```
   Tyr Gln Ser His Arg Asp Thr Ile Val Leu Leu Cys Lys Pro Glu Pro
           515                 520                 525

   Glu Leu Asn Ala Ala Ile Pro Ser Ala Asn Pro Ala Lys Thr Met Gln
           530                 535                 540

 5 Gly Ser Glu Val Val Asn Val Leu Lys Ser Leu Leu Ser Asn Leu Asp
           545                 550                 555                 560

   Glu Val Lys Lys Glu Arg Glu Gly Leu Glu Asn Asp Leu Lys Ser Val
           565                 570                 575

   Asn Phe Asp Met Thr Ser Lys Phe Leu Thr Ala Leu Ala Gln Asp Gly
           580                 585                 590

10 Val Ile Asn Glu Glu Ala Leu Ser Val Thr Glu Leu Asp Arg Val Tyr
           595                 600                 605

   Gly Gly Leu Thr Thr Lys Val Gln Glu Ser Leu Lys Lys Gln Glu Gly
           610                 615                 620

15 Leu Leu Lys Asn Ile Gln Val Ser His Gln Glu Phe Ser Lys Met Lys
           625                 630                 635                 640

   Gln Ser Asn Asn Glu Ala Asn Leu Arg Glu Glu Val Leu Lys Asn Leu
           645                 650                 655

   Ala Thr Ala Tyr Asp Asn Phe Asn Val Glu Leu Val Ala Asn Leu Lys Glu
           660                 665                 670

20 Gly Thr Lys Phe Tyr Asn Glu Leu Thr Glu Ile Leu Val Arg Phe Gln
           675                 680                 685

   Asn Lys Cys Ser Asp Ile Val Phe Ala Arg Lys Thr Glu Arg Asp Glu
           690                 695                 700
```

```
   Leu Leu Lys Asp Leu Gln Gln Ser Ile Ala Arg Glu Pro Ser Ala Pro
           705                 710                 715                 720

   Ser Ile Pro Thr Pro Ala Tyr Gln Ser Ser Pro Ala Gly Gly His Ala
           725                 730                 735

 5 Pro Thr Pro Pro Thr Ala Pro Arg Thr Met Pro Thr Lys Pro
           740                 745                 750

   Gln Pro Pro Ala Arg Pro Pro Pro Val Leu Pro Ala Asn Arg Ala
           755                 760                 765

   Pro Ser Ala Thr Ala Pro Ser Pro Val Gly Ala Gly Thr Ala Ala Pro
           770                 775                 780

10 Ala Pro Ser Gln Thr Pro Gly Ser Ala Pro Pro Gln Ala Gln Gly
           785                 790                 795                 800

   Pro Pro Tyr Pro Thr Tyr Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro
           805                 810                 815

15 Met Pro Met Gly Tyr Asn Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro
           820                 825                 830

   Tyr Pro Pro Val Tyr His Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly
           835                 840                 845

   Pro Gln Gln Pro Ser Tyr Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr
20         850                 855                 860

   Tyr Pro Gln Gln
           865
```

<210> 105
<211> 280
<212> PRT
<213> Homo sapiens
<220>
<221> Similar to four and a half LIM domains 3
<222> (1)..(280)
<223> Accession No. as of 29 August 2003: Q9BVA2
<400> 105

Met Ser Glu Ser Phe Asp Cys Ala Lys Cys Asn Glu Ser Leu Tyr Gly
1   5   10   15

Arg Lys Tyr Ile Gln Thr Asp Ser Gly Pro Tyr Cys Val Pro Cys Tyr
      20   25   30

Asp Asn Thr Phe Ala Asn Thr Cys Ala Glu Cys Gln Gln Leu Ile Gly
      35   40   45

His Asp Ser Arg Glu Leu Phe Tyr Glu Asp Arg His Phe His Glu Gly
50   55   60

Cys Phe Arg Cys Cys Arg Cys Gln Arg Ser Leu Ala Asp Glu Pro Phe
65   70   75   80

Thr Cys Gln Asp Ser Glu Leu Leu Cys Asn Asp Cys Tyr Cys Ser Ala
      85   90   95

Phe Ser Ser Gln Cys Ser Ala Cys Gly Glu Thr Val Met Pro Gly Ser
100   105   110

Arg Lys Leu Glu Tyr Gly Gly Gln Thr Trp His Glu His Cys Phe Leu
      115   120   125

Cys Ser Gly Cys Glu Gln Pro Leu Gly Ser Arg Ser Phe Val Pro Asp
130   135   140

5 Lys Gly Ala His Tyr Cys Val Pro Cys Tyr Glu Asn Lys Phe Ala Pro
145   150   155   160

Arg Cys Ala Arg Cys Ser Lys Thr Leu Thr Gln Gly Gly Val Thr Tyr
      165   170   175

Arg Asp Gln Pro Trp His Arg Glu Cys Leu Val Cys Thr Gly Cys Gln
10 180   185   190

Thr Pro Leu Ala Gly Gln Gln Phe Thr Ser Arg Asp Glu Asp Pro Tyr
      195   200   205

Cys Val Ala Cys Phe Gly Glu Leu Phe Ala Pro Lys Cys Ser Ser Cys
210   215   220

15 Lys Arg Pro Ile Val Gly Leu Gly Gly Gly Lys Tyr Val Ser Phe Glu
225   230   235   240

Asp Arg His Trp His His Asn Cys Phe Ser Cys Ala Arg Cys Ser Thr
245   250   255

Ser Leu Val Gly Gln Gly Phe Val Pro Asp Gly Asp Gln Val Leu Cys
20 260   265   270

Gln Gly Cys Ser Gln Ala Gly Pro
275   280

<210> 106
<211> 280
<212> PRT
<213> Homo sapiens

<220>

<221> Skeletal muscle LIM-protein 2 (SLIM 2)

<222> (1)..(280)

<223> Accession No. as of 29 August 2003: Q13643

<400> 106

```
Met Ser Glu Ser Phe Asp Cys Ala Lys Cys Asn Glu Ser Leu Tyr Gly
1               5                   10                  15

Arg Lys Tyr Ile Gln Thr Asp Ser Gly Pro Tyr Cys Val Pro Cys Tyr
            20                  25                  30

Asp Asn Thr Phe Ala Asn Thr Cys Ala Glu Cys Gln Gln Leu Ile Gly
        35                  40                  45

His Asp Ser Arg Glu Leu Phe Tyr Glu Asp Arg His Phe His Glu Gly
    50                  55                  60

Cys Phe Arg Cys Arg Cys Gln Arg Ser Leu Ala Asp Glu Pro Phe
65                  70                  75                  80

Thr Arg Gln Asp Ser Glu Leu Leu Cys Asn Asp Cys Tyr Cys Ser Ala
            85                  90                  95

Phe Ser Ser Gln Cys Ser Ala Cys Gly Glu Thr Val Met Pro Gly Ser
        100                 105                 110
```

```
Arg Lys Leu Glu Tyr Gly Gly Gln Thr Trp His Glu His Cys Phe Leu
                115                 120                 125

Cys Ile Gly Cys Glu Gln Pro Leu Gly Ser Arg Ser Phe Val Pro Asp
            130                 135                 140

Lys Gly Ala His Tyr Cys Val Pro Cys Tyr Glu Asn Asn Phe Ala Pro
5           145                 150                 155                 160

Arg Cys Ala Arg Cys Thr Lys Thr Leu Thr Gln Gly Gly Leu Thr Tyr
                165                 170                 175

Arg Asp Leu Pro Trp His Pro Lys Cys Leu Val Cys Thr Gly Cys Gln
10              180                 185                 190

Thr Pro Leu Ala Gly Gln Gln Phe Thr Ser Arg Asp Glu Asp Pro Tyr
                195                 200                 205

Cys Val Ala Cys Phe Gly Leu Phe Ala Pro Lys Cys Ser Ser Cys
                210                 215                 220

Lys Arg Pro Ile Val Gly Leu Gly Gly Lys Tyr Val Ser Phe Glu
15              225                 230                 235                 240

Asp Arg His Trp His Asn Cys Phe Thr Cys Asp Arg Cys Ser Asn
                245                 250                 255

Ser Leu Val Gly Gln Gly Phe Pro Asp Gly Asp Gln Val Leu Cys
                260                 265                 270

Gln Gly Cys Ser Gln Ala Gly Pro
20              275                 280
```

<210> 107
<211> 133
<212> PRT
<213> Homo sapiens
<220>
<221> Cytochrome b5
<222> (1)..(133)
<223> Accession No. as of 29 August 2003: P00167
<400> 107

Ala Glu Gln Ser Asp Glu Ala Val Lys Tyr Tyr Thr Leu Glu Glu Ile
1   5   10   15

Gln Lys His Asn His Ser Ser Lys Ser Trp Trp Leu Ile Leu His His Lys
            20   25   30

Val Tyr Asp Leu Thr Lys Phe Leu Glu Glu His Pro Gly Gly Glu Glu
        35   40   45

Val Leu Arg Glu Gln Ala Gly Gly Asp Ala Thr Glu Asn Phe Glu Asp
    50   55   60

Val Gly His Ser Thr Asp Ala Arg Glu Met Ser Lys Thr Phe Ile Ile
65   70   75   80

Gly Glu Leu His Pro Asp Asp Arg Pro Lys Leu Asn Lys Pro Pro Glu
            85   90   95

Thr Leu Ile Thr Ile Asp Ser Ser Ser Trp Trp Thr Asn Trp
        100   105   110

Val Ile Pro Ala Ile Ser Ala Val Ala Val Ala Leu Met Tyr Arg Leu
                115   120   125

Tyr Met Ala Glu Asp
                130

<210> 108
<211> 175
<212> PRT
<213> Homo sapiens
<220>
<221> Pancreatitis-associated protein 1 precursor
<222> (1)..(175)
<223> Accession No. as of 29 August 2003: Q06141
<400> 108

Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu Ser
1   5   10   15

Cys Leu Met Leu Leu Ser Gln Val Gln Gly Glu Glu Pro Gln Arg Glu
            20   25   30

Leu Pro Ser Ala Arg Ile Arg Cys Pro Lys Gly Ser Lys Ala Tyr Gly
        35   40   45

Ser His Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser Trp Thr Asp Ala
    50   55   60

```
Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Asn Leu Ser Val Leu
        65              70                  75              80

Ser Gly Ala Glu Gly Ser Phe Val Ser Ser Leu Val Lys Ser Ile Gly
                    85              90                  95

Asn Ser Tyr Ser Tyr Val Trp Ile Gly Leu His Asp Pro Thr Gln Gly
5               100             105                 110

Thr Glu Pro Asn Gly Glu Gly Trp Glu Trp Ser Ser Ser Asp Val Met
            115                 120                 125

Asn Tyr Phe Ala Trp Glu Arg Asn Pro Ser Thr Ile Ser Ser Pro Gly
10      130                 135                 140

His Cys Ala Ser Leu Ser Arg Ser Thr Ala Phe Leu Arg Trp Lys Asp
            145                 150             155             160

Tyr Asn Cys Asn Val Arg Leu Pro Tyr Val Cys Lys Phe Thr Asp
            165                 170             175

15
```

<210> 109
<211> 1028
<212> PRT
<213> Homo sapiens
<220>
<221> Collagen alpha 1(VI) chain precursor
<222> (1)..(1028)
<223> Accession No. as of 29 August 2003: P12109

<400> 109

```
Met Arg Ala Ala Arg Ala Leu Leu Pro Leu Leu Gln Ala Cys Trp
1               5                   10                  15

Thr Ala Gln Asp Glu Pro Glu Thr Pro Arg Ala Val Ala Phe Gln
            20                  25                  30

Asp Cys Pro Val Asp Leu Phe Phe Val Leu Asp Thr Ser Glu Ser Val
        35                  40                  45

Ala Leu Arg Leu Lys Pro Tyr Gly Ala Leu Val Asp Lys Val Lys Ser
10          50                  55                  60

Phe Thr Lys Arg Phe Ile Asp Asn Leu Arg Asp Arg Tyr Arg Cys
            65                  70              75              80

Asp Arg Asn Leu Val Trp Asn Ala Gly Ala Leu His Tyr Ser Asp Glu
            85                  90                  95

Val Glu Ile Ile Gln Gly Leu Thr Arg Met Pro Gly Gly Arg Asp Ala
15          100                 105                 110

Leu Lys Ser Ser Val Asp Ala Val Lys Tyr Phe Gly Lys Gly Thr Tyr
            115                 120                 125

Thr Asp Cys Ala Ile Lys Lys Gly Leu Glu Gln Leu Leu Val Gly Gly
            130                 135                 140

Ser His Leu Lys Glu Asn Lys Tyr Leu Ile Val Val Thr Asp Gly His
20          145                 150             155             160

Pro Leu Glu Gly Tyr Lys Glu Pro Cys Gly Gly Leu Glu Asp Ala Val
            165                 170             175
```

```
    Asn Glu Ala Lys His Leu Gly Val Lys Val Phe Ser Val Ala Ile Thr
                    180             185             190

    Pro Asp His Leu Glu Pro Arg Leu Ser Ile Ile Ala Thr Asp His Thr
                    195             200             205

    Tyr Arg Arg Asn Phe Ala Ala Asp Trp Gly Gln Ser Arg Asp Ala
5                   210             215             220

    Glu Glu Ala Ile Ser Gln Thr Ile Asp Thr Ile Val Asp Met Ile Lys
            225             230             235             240

    Asn Asn Val Glu Gln Val Cys Cys Ser Phe Glu Cys Gln Pro Ala Arg
10                  245             250             255

    Gly Pro Pro Gly Leu Arg Gly Asp Pro Gly Phe Glu Gly Glu Arg Gly
                    260             265             270

    Lys Pro Gly Leu Pro Gly Glu Lys Gly Glu Ala Gly Asp Pro Gly Arg
                    275             280             285

    Pro Gly Asp Leu Gly Pro Val Gly Tyr Gln Gly Met Lys Gly Glu Lys
15                  290             295             300

    Gly Ser Arg Gly Glu Lys Gly Ser Arg Gly Pro Lys Gly Tyr Lys Gly
            305             310             315             320

    Glu Lys Gly Lys Lys Arg Gly Ile Asp Gly Val Asp Gly Val Lys Gly Glu
                    325             330             335

20  Met Gly Tyr Pro Gly Leu Pro Gly Cys Lys Gly Ser Pro Gly Phe Asp
                    340             345             350

    Gly Ile Gln Gly Pro Pro Gly Pro Lys Gly Asp Pro Gly Ala Phe Gly
                    355             360             365
```

```
    Leu Lys Gly Glu Lys Gly Glu Pro Gly Ala Asp Gly Glu Ala Gly Arg
                    370             375             380

    Pro Gly Ala Arg Gly Pro Ser Gly Asp Glu Gly Pro Ala Gly Glu Pro
            385             390             395             400

5   Gly Pro Pro Gly Glu Lys Gly Glu Ala Gly Asp Glu Gly Asn Pro Gly
                    405             410             415

    Pro Asp Gly Ala Pro Gly Glu Arg Gly Gly Pro Gly Glu Arg Gly Pro
                    420             425             430

    Arg Gly Thr Pro Gly Pro Arg Gly Pro Arg Gly Asp Pro Gly Glu Ala
10                  435             440             445

    Gly Pro Gln Gly Asp Gln Gly Arg Gly Gly Pro Val Gly Val Pro Gly
                    450             455             460

    Asp Pro Gly Glu Ala Gly Pro Ile Gly Pro Lys Gly Tyr Arg Gly Asp
            465             470             475             480

15  Glu Gly Pro Pro Gly Ser Glu Gly Ala Arg Gly Ala Pro Gly Pro Ala
                    485             490             495

    Gly Pro Pro Gly Asp Pro Gly Leu Met Gly Glu Arg Gly Glu Asp Gly
                    500             505             510

    Pro Ala Gly Asn Gly Thr Glu Gly Phe Pro Gly Phe Pro Gly Tyr Pro
                    515             520             525

20  Gly Asn Arg Gly Ala Pro Gly Ile Asn Gly Thr Lys Gly Tyr Pro Gly
                    530             535             540

    Leu Lys Gly Asp Glu Gly Glu Ala Gly Asp Pro Gly Asp Asp Asn Asn
            545             550             555             560
```

Asp Ile Ala Pro Arg Gly Val Lys Gly Ala Lys Gly Tyr Arg Gly Pro
565   570   575

Glu Gly Pro Gln Gly Pro Pro Gly His Gln Gly Pro Pro Gly Pro Asp
580   585   590

5   Glu Cys Glu Ile Leu Asp Ile Ile Met Lys Met Cys Ser Cys Cys Glu
595   600   605

Cys Lys Cys Gly Pro Ile Asp Leu Leu Phe Val Leu Asp Ser Ser Glu
610   615   620

10 Ser Ile Gly Leu Gln Asn Phe Glu Ile Ala Lys Asp Phe Val Val Lys
625   630   635   640

Val Ile Asp Arg Leu Ser Arg Asp Glu Leu Val Lys Phe Glu Pro Gly
645   650   655

Gln Ser Tyr Ala Gly Val Val Gln Tyr Ser His Ser Gln Met Gln Glu
660   665   670

15 His Val Ser Leu Arg Ser Pro Ser Ile Arg Asn Val Gln Glu Leu Lys
675   680   685

Glu Ala Ile Lys Ser Leu Gln Trp Met Ala Gly Gly Thr Phe Thr Gly
690   695   700

Glu Ala Leu Gln Tyr Thr Arg Asp Gln Leu Leu Pro Pro Ser Pro Asn
705   710   715   720

20 Asn Arg Ile Ala Leu Val Ile Thr Asp Gly Arg Ser Asp Thr Gln Arg
725   730   735

Asp Thr Thr Pro Leu Asn Val Leu Cys Ser Pro Gly Ile Gln Val Val
740   745   750

Ser Val Gly Ile Lys Asp Val Phe Asp Val Phe Ile Pro Gly Ser Asp Gln
755   760   765

Leu Asn Val Ile Ser Cys Gln Gly Ala Pro Ser Gln Gly Arg Pro
770   775   780

5   Gly Leu Ser Leu Val Lys Glu Asn Tyr Ala Glu Leu Leu Glu Asp Ala
785   790   795   800

Phe Leu Lys Asn Val Thr Ala Gln Ile Cys Ile Asp Lys Lys Cys Pro
805   810   815

Asp Tyr Cys Pro Ile Thr Phe Ser Ser Pro Ala Asp Ile Thr Ile
820   825   830

10 Leu Leu Asp Gly Ser Ala Ser Val Gly Ser His Asn Phe Asp Thr Thr
835   840   845

Lys Arg Phe Ala Lys Arg Leu Ala Glu Arg Phe Leu Thr Ala Gly Arg
850   855   860

15 Thr Asp Pro Ala His Asp Val Arg Val Ala Val Val Gln Tyr Ser Gly
865   870   875   880

Thr Gly Gln Gln Arg Pro Glu Arg Ala Ser Leu Gln Phe Leu Gln Asn
885   890   895

20 Tyr Thr Ala Leu Ala Ser Ala Val Asp Ala Met Asp Phe Ile Asn Asp
900   905   910

Ala Thr Asp Val Asn Asp Ala Leu Gly Tyr Val Thr Arg Phe Tyr Arg
915   920   925

Glu Ala Ser Ser Gly Ala Ala Lys Lys Arg Leu Leu Phe Ser Asp
930   935   940

Met Ser Leu Ser Ala Phe Leu Phe Leu Ala Leu Ile Gly Gly Thr
1   5   10   15

Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln
      20   25   30

5 Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro
      35   40   45

Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val
      50   55   60

Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His
10 65   70   75   80

Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile
      85   90   95

Leu Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe
      100   105   110

15 Ser Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu
      115   120   125

Thr Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu
      130   135   140

Thr His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn
20 145   150   155   160

Leu Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val
      165   170   175

Ser Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser
      180   185   190

Gly Asn Ser Gln Gly Ala Thr Pro Ala Ala Ile Glu Lys Ala Val Gln
945   950   955   960

Glu Ala Gln Arg Ala Gly Ile Glu Ile Phe Val Val Val Gly Arg
      965   970   975

5 Gln Val Asn Glu Pro His Ile Arg Val Leu Val Thr Gly Lys Thr Ala
      980   985   990

Glu Tyr Asp Val Pro Tyr Gly Glu Ser His Leu Phe Arg Val Pro Ser
      995   1000   1005

Tyr Gln Ala Leu Leu Arg Gly Val Phe His Gln Thr Val Ser Arg
      1010   1015   1020

10 Lys Val Ala Leu Gly
      1025

15   <210> 110

  <211> 338

  <212> PRT

  <213> Homo sapiens

  <220>

20 <221> Lumican precursor

  <222> (1)..(338)

  <223> Accession No. as of 29 August 2003: P51884

  <400> 110

Phe Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu
                195   200   205

Thr Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr
            210   215   220

5   Phe Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu
    225   230   235   240

    Leu Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu
                    245   250   255

    Val Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val
10   260   265   270

    Asn Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys
                275   280   285

    Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser
            290   295   300

15 Lys Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Glu Thr Ser
    305   310   315   320

    Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val Ala Asn Glu Val Thr
                    325   330   335

    Leu Asn

20